

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 184522

TO: Celine Qian

Location: REM/2A64/2C70

Art Unit: 1636

Tuesday, April 11, 2006

Case Serial Number: 10/696708

From: Kristine Hensle

Location: Biotech-Chem Library

REM-1B69

Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Qian,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle Librarian STIC Biotech/Chem Library (571)272-4161



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CRFE

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Names	Celino Qia	n	Examiner #:	78710	Date: 4/6	5/06
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Location (Bldg/Room#): ********	2464 (Mailbox #):	2670	Results Format P	referred inical	lal ADED	DICK
To ensure an efficient and qua	ality search, please attach a	copy of the co	ver sheet, claims, and	abstract or fill	out the following	ng:
Title of Invention:	nutations in	and	Genomi	Structu	re of	HERG
Inventors (please provide f						
Earliest Priority Date:	7/27/1998			<u> </u>		
Search Topic: Please provide a detailed statem Plected species or structures, key Define any terms that may have	ent of the search topic, and pwords, synonyms, acronym	describe as spe	numbers, and combine	with the concen	to be searched, of or utility of th	Include the winder invention.
For Sequence Searches Only* ppropriate serial number.		2			fif numbers) ale	ong with the
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11 US-11-245-147-174

5 US-09-925-065A-473258

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Sequence 413820,
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ALIGNMENTS	US-11-136-527-6416 US-10-909-125-814 US-09-925-065A-727546 US-11-136-527-2320 US-11-077-716-1 US-11-249-873-1 US-11-249-873-1 US-11-249-873-2 US-11-249-873-2 US-11-249-873-4 US-11-249-873-4	US-09-925-065A-423156 US-10-301-480-1100919 US-10-301-480-1100919 US-10-301-480-14469 US-10-301-480-654878 US-09-925-065A-451154 US-09-925-065A-451154 US-10-301-480-510257 US-10-301-480-1123666 US-10-714-887-123	US-10-955-054A-50 US-10-750-185-34096 US-10-750-623-34096 US-11-121-086-26 US-11-136-527-303211 US-10-995-561-80702
	Sequence 6416, App Sequence 814, App Sequence 727546, Sequence 2320, Ap Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 479, App	Sequence 423156, Sequence 487510, Sequence 1100919, Sequence 41469, A Sequence 654878, Sequence 451154, Sequence 510257, Sequence 1123666, Sequence 123, App	Sequence 50, Appl Sequence 34096, A Sequence 34096, A Sequence 26, Appl Sequence 1690, Ap Sequence 303211, Sequence 80702, A

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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 413820
LENGTH: 639
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-413820
RESULT 2
US-10-301-480-479809/c
; Sequence 479809, Application US/10301480
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Best Local 9
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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US-10-301-480-1093218
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TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-479809
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TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: in the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 479809
                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
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TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
CURRENT FILING DATE: 2002-11-21
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94.4%;
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Pred. No. 2.1e+02;
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Pred. No. 2.1e+02;
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US-10-301-480-125704/c
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; ORGANISM: Homo sapiens
US-09-925-065A-24467
                                                                                                                                                                                                                                                                                    US-10-301-480-739113/c
Sequence 739113, Application US/10301480

Publication No. US20060057564A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: in the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10
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SEQ ID NO 125704
LENGTH: 503
TYPE: DNA
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Best Local :
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
PILE REFERENCE: 106827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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Local Similarity 89.5%;
es 17; Conservativo
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APPLICATION NUMBER: US 60/252,147
FILING DATE: 2000-11-20
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Pred. No. 4.1e.
0; Mismatches
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Pred. No. 4.1e+02;
0; Mismatches 2;
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RESULT 8
US-09-925-065A-473258
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                                              Sequence 473258, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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Best Local S
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PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PACENTIN Ver. 3.2
SEQ ID NO 174
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 739113
LENGTH: 503
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APPLICANT:
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TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
TILLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
TILLE OF INVENTION OF USE
PRIOR APPLICATION NUMBER: PCT/IB02/02211
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
               PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: Homo sapiens elastin microfibril interface located OTHER INFORMATION: protein (EMILIN), mRNA
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PRIOR APPLICATION NUMBER: US 60/252,147
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TYPE: DNA
ORGANISM: Homo sapiens
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17; Conserv
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CALL, KATHERINE
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Pred. No. 3.4e+02;
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Pred. No. 4.1e+02;
0; Mismatches 2
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Sequence 586930, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLS OF INVENTION: Identification and Mapping of Single
TITLS OF INVENTION: Nucleotide Polymorphisms in the Human Genome
PILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/251,766
PRIOR PILING DATE: 2001-01-16
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US-10-301-480-586930
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; ORGANISM: Homo sapiens
US-09-925-065A-473258
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PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
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Matches
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Local Similarity 94.1%;
es 16; Conservation
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nes 16; Conserv
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Pred. No. 6.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.4; DB 6;
Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.3e+02;
                                                                                              of Single Nucleotide Polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 566;
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-11-055-822-333
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; ORGANISM: Homo sapien
US-10-301-480-1200339
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; ORGANISM: Homo sapien
US-10-301-480-586930
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PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 586930
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows SEQ ID NO 1200339
                                                                                                                                                                                                                                                                                                                 Sequence 333, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                     APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schoder, Hartwig
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
                FILE REFERENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 988
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APPLICATION NUMBER: 60/142,101
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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94.1%;
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Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Single Nucleotide Polymorphisms
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APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT APPLICATION NUMBER: 09/666,740
PRIOR APPLICATION NUMBER: 09/666,740
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR APPLICATION NUMBER: 60/143,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR PILING DATE: 1909-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR PILING DATE: 1909-08-12
PRIOR PILING DATE: 1909-08-03-09
PRIOR PILING DATE: 1909-08-05-08
PRIOR PILING DAT
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US-11-055-822-59
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NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 333
LENGTH: 1080
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhar
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                                                                   PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                          PRIOR
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PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE
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LOCATION: (101)..(1057)
OTHER INFORMATION: RXA02158
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APPLICATION NUMBER: 60/
FILING DATE: 1999-08-12
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APPLICATION NUMBER: DE 19931418.7
FILING DATE: 1999-07-08
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APPLICATION NUMBER: DE 19931420.9
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Prior Application data removed - SEQ ID NOS: 1158
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Zelder, Oskar
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Pred. No. 5.
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                                         See File Wrapper or PALM
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                                                                                                                                                                                                                                                             SEQ ID NO 299
LENGTH: 1296
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                                                                    Matches
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Best Local
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/606,740 PRIOR FILING DATE: 2000-06-23 PRIOR APPLICATION NUMBER: 60/141,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: DE PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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APPLICANT: Kroger, Burkhar
                                                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1273)
OTHER INFORMATION: RXS02157
                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Corynebacterium glutamicum
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NAME/KEY: CDS
LOCATION: (101)..(1273)
OTHER INFORMATION: RXS02157
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LENGTH: 1296
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A APPLICATION NUMBER: 60/148,613

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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: DE 19931415.2
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931418.7
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CURRENT APPLICATION NUMBER: US/11/055,822

CURRENT FILING DATE: 2005-06-21

PRIOR APPLICATION NUMBER: 09/606,740

PRIOR PILING DATE: 1999-06-25

PRIOR PILING DATE: 1999-06-25

PRIOR PILING DATE: 1999-07-02

PRIOR PILING DATE: 1999-07-03

PRIOR APPLICATION NUMBER: 60/148,613

PRIOR PILING DATE: 1999-08-12

PRIOR PILING DATE: 1999-08-12

PRIOR PILING DATE: 1999-07-01

PRIOR PILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19930476.9

PRIOR APPLICATION NUMBER: DE 19931415.2

PRIOR PILING DATE: 1999-07-08

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APPLICANT: Haberhauer, Gregor

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTETURE
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.0 1008 3 US-09-815-242-8010 Sequence 8010, 1788 7 US-10-437-963-5286 Sequence 10345, 20348 7 US-10-337-963-10345 Sequence 10345, 2038 8 US-10-326-055A-25 Sequence 106, 2763 6 US-10-236-055A-25 Sequence 25, Al Sequence 25, Al Sequence 270, Al Sequence 2714, 20367 9 US-10-852-335A-70 Sequence 2714, 20367 9 US-10-852-3319 Sequence 3319, 203846 3 US-09-764-877-3319 Sequence 3319, 203864 3 US-09-764-877-3320 Sequence 3320, 203864 5 US-10-242-515-3320 Sequence 3320, 203864 5 US-10-242-515-3320 Sequence 1027, 2039768 5 US-10-087-192-1037 Sequence 1037, 2039768 5 US-10-087-192-1037 Sequence 1030, 203976 5 US-10-087-192-1030 Sequence 1030, 203976 5 US-10-424-599-105108 Sequence 2738, 203977596 Sequence 2738, 203977596 Sequence 21494, 20368 4 US-09-25-065A-473259 Sequence 473259, 20366 4 US-09-925-065A-473259 Sequence 473259	15.4	15.4								•	•										15.8	15.8
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ALIGNMENTS

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RESULT 2
US-10-696-708-61
Sequence 61, Application US/10696708
Sequence 61, Application US/10696708
Publication No. US20040078833A1
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Splaweki, Igor
TITTLE OF INVENTION: MUTATIONS IN AND GENOMIC
TITTLE OF INVENTION: SYNDROME GENE
FILE REFERENCE: 3233-164
CURRENT APPLICATION NUMBER: US/10/696,708
CURRENT APPLICATION NUMBER: US 09/735,995
PRIOR APPLICATION NUMBER: US 09/735,995
PRIOR FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 61, Application US/09735995
Patent No. US20010034024A1
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
ITILE OF INVENTION: MUTATIONS IN AND GENOMIC
ITILE OF INVENTION: MUTATIONS IN AND GENOMIC
CURRENT APPLICATION NUMBER: US/09/735,995
CURRENT APPLICATION NUMBER: US/09/735,995
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/226,012
PRIOR APPLICATION NUMBER: 09/226,012
PRIOR PILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-995-61
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Best Local S
Matches 20
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Pred. No. 13;
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; SEQ ID NO 14963
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-14963
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; ORGANISM: Homo sapiens
US-10-696-708-61
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PRIOR APPLICATION NUMBER: 09/12
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61
LENGTH: 20
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US-10-027-632-14963/c
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PRIOR FILLING DATE: 2000-04-20
PRIOR PELLUNG DATE: 2000-03-29
PRIOR FILLING DATE: 2000-03-29
PRIOR PELLUNG DATE: 2000-02-24
PRIOR PILLING DATE: 2000-02-24
PRIOR PELLUNG DATE: 1999-11-23
PRIOR PILLING DATE: 1999-11-23
PRIOR PILLING DATE: 1999-09-28
PRIOR PILLING DATE: 1999-09-28
PRIOR PILLING DATE: 1999-09-28
Sequence 14963, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14963, Application US/10027632 Publication No. US20020198371A1
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
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SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 38
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2011-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 5165
LENGTH: 897
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                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)..(897)
US-10-156-761-5165
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US-10-156-761-5165
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PRIOR FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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Matches 19; Conserv
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SEQ ID NO 14963
LENGTH: 477
                                                                              Matches
                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Streptomyces avermitilis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                429 TTGACACCGCCCCTGGTCGT 410
                                                                              18;
                          TTGACCCCGCCCCTGGTCG 19
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rrcaccccccccccrccrcc 826
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94.7%;
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Pred. No. 3
                                                                                                Score 17.4;
Pred. No. 99
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RESULT 6 US-10-156-761-1 ; Sequence 1, Application US/10156761

Publication No. US20030119018A1

INFORMATION:

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TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants | FILE REFERENCE: 38-21(5322)B | CURRENT APPLICATION NUMBER: US/10/425,115 | CURRENT FILING DATE: 2003-04-28 | NUMBER OF SEQ ID NOS: 369326 | SEQ ID NO 97440 | SEQ ID NO 97440 | CRORANISM: Zea mays | CRORANISM: Z
RESULT 8
US-10-282-122A-7484/c
; Sequence 7484, Application US/10282122A
; Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: MRT4577_2037C.1 US-10-425-115-97440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION UNMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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NAME/KEY: misc feature
LOCATION: (4187715)
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                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                         1 TTGACCCCGCCCCTGGTCGT 20
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18; Conserv
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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Cao, Yongwei
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90.0%;
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Pred. No. 2.4e+02;
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Pred. No. 19
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 61568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
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US-10-425-115-61568/c
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7484
                                                                                                                                                                                                                                                                                                        Sequence 61568, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
APPLICANT:
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TYPE: DNA
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Local Similarity 90.0%;
nes 18; Conservative
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
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Carr, Grant
Yamamoto, Robe:
Forsyth, R.
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Zyskind, Judith
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Pred. No. 1.8e+02;
0; Mismatches 2;
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RESULT 11
US-10-425-115-152918
; Sequence 152918, Application US/10425115
; Publication No. US20040214272A1
; Publication No. US20040214272A1
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US-09-925-065A-413820/c
US-09-925-065A-413820, Application US/09925065A
; Sequence 413820, Application US/09925065A
; Publication No. US20050228172A9
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; ORGANISM: Homo sapiens
US-09-925-065A-413820
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                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovallo, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
                                                             NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 152918
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                    CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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                        LENGTH: 826
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 639
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94.4%;
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Pred. No. 3.1e+02;
0; Mismatches 1;
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; OTHER INFORMATION: Clone ID: LIB3608-041-A7_FLI US-10-425-114-24374
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US-10-425-114-24374
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                                                        TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 24374
LENGTH: 1124
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
FEATURE: The May of the Molecules and Other Molecules Associated Ass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24374, Application US/10425114
Publication No. US20040034888A1
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LENGTH: 890
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi
APPLICANT: Screen, Steve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 73128
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OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_71044C.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: UC-ZMFLMO17223B10_FLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36
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Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
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Pred. No. 2.9e+02;
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Pred. No. 2.9e+02;
0; Mismatches 1;
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 21303
LENGTH: 1483
TYPE: DNA
OTHER INFORMATION: Clone ID: LIB3279-223-C11_FLI
US-10-425-114-21303
                                                                                                                          APPLICANT: OWNER, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHAKKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2011-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4733
LENGTH: 1644
; NAME/KEY: CDS
; LOCATION: (1)..(1644)
US-10-156-761-4733
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US-10-425-114-21303
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US-10-156-761-4733
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Publication No. US20040034888A1
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Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                   TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                FEATURE:
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Query Match 82.0%; Score 16.4; DB 6; Length 1644;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 2 TGACCCCGCCCCTGGTCG 19

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Db 65 TGACCCCGCACCTGGTCG 82
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2965, Ap
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2905, Appl
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271, Ap
2301, Ap
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2611, Ap
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Fatent No. 6207383
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Splawaki, Igor
ITILE OF INVENTION: MUTATIONS IN AND GENOMIC
ITILE OF INVENTION: MUTATIONS IN AND GENOMIC
CURRENT APPLICATION NUMBER: US/09/226,012
CURRENT APPLICATION NUMBER: US/09/226,012
CURRENT APPLICATION NUMBER: 09/122,847
EARLIER APPLICATION NUMBER: 09/122,847
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-226-012-61
RESULT 2
US-09-252-991A-3069/c
US-09-252-991A-3069/c
; Sequence 3069, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
APPLICANT: MATC J. RUBenfield et al.
APPLICANT: MATC J. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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US-09-226-012-61
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US-09-949-016-12390

US-09-621-976-19114

US-09-824-133-142

US-09-949-016-184859

US-09-949-016-184859

US-09-949-016-185013

US-09-949-016-185013

US-09-949-016-185013

US-09-949-016-185014

US-09-949-016-185014

US-09-949-016-185019

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US-09-949-016-13232

US-09-949-016-13232
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2905
ENGTH: 1617
5
                                                                                                                   ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2905
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2966
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LENGTH: 1026
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Best Local
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Best Local Similarity
                                            Matches
                                                           Query Match
Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND ANNO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARBUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                          18; Conservative
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       TTGACCCCGCCCCTGGTCGT 20
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Pred. No. 1.1e+02;
                                                           Score 16.8; DB 3;
Pred. No. 1.1e+02;
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; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 25
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-25
                                                                                                RESULT 7
US-09-134-001C-27/c
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US-09-134-001C-25
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US-09-252-991A-3301
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                  GENERAL INFORMATION:
APPLICANT: Lynn Dou
                                                          Sequence 27, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                Best Local Similarity
Matches 17; Conserv
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LENGTH: 501
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APPLICANT: Marc J.
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TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR REPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND
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ORGANISM: Pseudomonas aeruginosa
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les 17; Conserva
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  AMINO ACID SEQUENCES RELATING
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FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 27

LENGTH: 819
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US-09-252-991A-2301
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NUMBER OF SEQ ID NOS:
SEQ ID NO 2301
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Best Local
                                                                                    FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
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                                            PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1998-07-27
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TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Similarity 89.5%;
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                                                                 US 60/094,190
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Pred. No. 3.1e+02;
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3234
LENGTH: 1965
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-2611/c
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Patent No. 6551795

PATENT INFORMATION:
GENERAL INFORMATION:
HOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: HUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEC IT NO SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Marc J.
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LENGTH: 1221
                                                              Matches
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                             Local Similarity
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1777
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17; Conservative
TGCCCCCGCCCGTGGTCGT 1795
                         TGACCCCGCCCCTGGTCGT
                                                           79.0%; ilarity 89.5%; Conservative
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Pred. No. 3.
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Pred. No. 3.1e+02;
0; Mismatches 2
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Pred. No. 3
                                                              Mismatches
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FILE REFERENCE: JHU1590
CURRENT APPLICATION NUMBER: US/09/398,522
CURRENT FILING DATE: 199-09-15
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 106
LENGTH: 2093
TYPE: DNA
ORGANISM: Homo Bapiens
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US-09-949-016-15601/c
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, NAME/KEY: gene
, LOCATION: (0)...(0)
, OTHER INFORMATION: CACNAIG CpG ISLAND
US-09-398-522-106
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US-09-252-991A-3413/c
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Sequence 15601, Application US/09949016

Retent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 106, Application US/09398522
Patent No. 6783933
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3413
LENGTH: 2325
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3413, Application US/09252991A Patent No. 6551795
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Best Local Similarity 89.5%;
Matches 17; Conservative
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TITLE OF INVENTION: CACNAIG POLYNUCLEOTIDE POLYPEPTIDE AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                              Local
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Pred. No. 3.2e+02;
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Search completed: April 10, 2006, 15:05:37 Job time: 77 secs

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; NUMBER OF SEQ ID NOS: 4096
; SOPTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 2337
; TYPE; DNA
; ORGANISM: Homo sapiens
US-10-104-047-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 15601
LENGTH: 70308
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                                                                                                                                                                                                                                                                                                                                                      Sequence 160, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
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                                                                                        Query Match 77.0%;
Best Local Similarity 94.1%;
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Best Local
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CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
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1599 TTGACCCCGCCCCTGAT 1583
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                 TTGACCCCGCCCCTGGT 17
                                                                      Conservative
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Pred. No. 4.8e+02;
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Maximum Match 100%
Listing first 45 s
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seq length: 2000000000
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Match Length
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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CC635423 OGVEL74TV	AI692069 606011D06	CX693482 ydc82c10.	CF646796 3530_1_32	BI894407 ga56b12.y	AI914370 wd48b06.x	CX561782 ydb58h03.	CD341478 StrPu536.	DR787771 ZM_BFb000	BH226705 1006134B0	AL688012 Fugu rubr	F35316 HSPD31376 H	CA028327 HZ61K11r	вн896258 3526_1_3_	вн896224 3526_1_3_	BF313573 601900212	CD048275 AGENCOURT	BM914898 AGENCOURT	DN702679 CLJ43-A09	BF684249 602141165	BZ805028 PUGCB39TB	BG032770 602298425	CG114553 PUFTI36TD

ALIGNMENTS

	. <u>.</u>				
	FEATURES source		AUTHORS TITLE JOURNAL COMMENT	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BX856785 LOCUS DEFINITION ACCESSION
/organism="Oncornynchus mykiss" /mol_type="mcNA" /db_xref="taxon:8022" /clone="tcba0005c.l.01" /tissue_type="multi-tissues" /dev_stage="from embryos to adults" /lab_host="pH108" /clone_lib="tcba" /clone_lib="tcba" /clone_lib="tcba" /note="vector: pT773D-pac; Rainbow trout multi-tissues - normalized + 1 subtraction; Clone distribution : AGENAE Resource centre. Francois PUMNI, Francois.Fiumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352,	Seq primer: M13R. Seq primer: M13R. Location/Qualifiers 1. 780	INRA - SCRIBE Campus de beaulieu, RENNES cedex, 35042, France Tel: 02.23.48.50.09 Fax: 02.23.48.50.20 Email: Yann.Guiguen@beaulieu.rennes.inra.fr Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this	Govoroun, M., Guiguen, Y. and Le Gac, F. Govoroun, M., Guiguen, Y. and Le Gac, F. Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss Unpublished (2003) On Dec 10:10:003 this sequence version replaced g1:39953963. Contact, G. 10:003 this	BX856785.2 GI:42753667 EST. Oncorhynchus mykiss (rainbow trout) Oncorhynchus mykiss Oncorhynchus mykiss Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Protacanthopterygii; Neopterygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.	780 bp mRNA linear EST 20-MAY-2004 BX856785 tcba Oncorhynchus mykiss cDNA clone tcba0005c.l.01 5prim, BX856785

Soderlund, C.

Smart, D.,

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REFERENCE
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mRNA sequence.
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10982 row: m column: 18
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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                                                                                                                                                                                                                                                        Conservative
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/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI_CGAp_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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/mol_type="mRNA"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                         90.0%;
                                                    sequence.
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                                                                   linear GSS 26-JUL-2005
genomic clone OC_Ba0088D18
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                                                                                                                                                                                                                                                                                                                                                                                  479 bp mRNA linear EST 21-JUCYMG2F07 Coprinus cinereus YMG medium exponentially growing mycelia cDNAs Coprinopsis cinerea cDNA, mRNA sequence. DR752859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza coarctata (Porteresia coarctata)
Oryza coarctata
Dryza coarctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhattoldae; Oryzeae; Oryza.
                                                                           Contact: Contact Contact Contact Contact Contact Contact Missouri State University Southeast Missouri State University Cape Girardeau,
                                                                                                                                                                                                                  Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Psathyrellaceae; Coprinopsis.

1 (bases 1 to 479)

Wilke, S.K., Carlson, M.D., Barr, C., Murphy, B., Peters, J.M., Guerrero, A.R., Gathman, A.C., Lilly, W.W., and Pukkila, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0088 row: D column: 18
Seg primer: TAA TAC GAC TCA CTA TAG
Class: BAC ends.
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Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson,
                                                                                                                                                              Expressed sequence tags from Coprinus cinereus (Coprinopsis cinerea) cDNAs, summer 2005
Unpublished (2005)
                                                                                                                                                                                                                                                                                                           Coprinopsis cinerea (Coprinus cinereus)
Coprinopsis cinerea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Sode:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rao, K., Luo, M., Jetty, R.,
                                                                                                                                             Contact: Gathman AC
                                                                                                                                                                                                                                                                                                                                                                 DR752859.1 GI:71045301
                                   Fax: 573 651 2382
Email: agathman@semo.edu.
                                                                     Tel: 5736512361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza coarctata"

/mol_type="genomic DNA"

/mbl_type="genomic DNA"

/db_xref="taxon:77588"

/clone="OC Ba008BD18"

/tissue_type="leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                  ocation/Qualifiers
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'note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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94.7%;
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Pred. No. 2.3e+03;
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EST 21-JUL-2005

0

Gaps

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Email: huenishi@affrc.go.jp

BST project with full-length enriched cDNA libraries carried out
Animal Genome Research program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan Tel: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., 7
Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a
derived from porcine full-length cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP153423 full-length enriched sv
                                                                                                                                                                                                                                                                                                                                                                        Vector sequences were eliminated by RepeatMasker version 2002/07/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hirohide Uenishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 32 (1), D484-D488 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (pig)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scrofa cDNA clone OVRM10124G10 5', mRNA sequence
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                                                                                                                                                                                                                                                                                                            crossmatch version 0.990319 quality bases were trimmed | Location/Qualifiers
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                         Conservative
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ovary"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Coprinus cinereus YMG medium exponentially growing mycelia cDNAs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Okayama7#130"
/db_xref="taxon:5346"
/dev_stage="vegetative monokaryotic mycelium"
/lab_host="B. coli XL10-Gold"
                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9823"
/clone="OVRM10124G10"
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/mol_type="mRNA"
                                                                                                                                                                 tissue_type="ovary"
dev_stage="adult"
                                                                                                                                                                                                                                                                        organism="Sus scrofa"
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Pred. No. 2.2e+03;
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                                                                                                                                                                                                                                                                                         18;
                                                         BH342931 665 bp DNA linear GSS 03-DEC-200 CH230-41L4.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-41L4, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 41 row: L column: 14
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,B., Overton,L., Russell,D., ClRiggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
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BH342931.1
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Brain"
/clone lib="CHOX1-230 Segment 1"
/clone lib="CHOX1-230 Segment 1"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
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                       GI:17273665
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genomic clone
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REFERENCE AUTHORS

COMMENT

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ORIGIN

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RESULT 5 BP153423 LOCUS

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ORIGIN

Query Match Best Local

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ACCESSION VERSION

KEYWORDS

SOURCE ORGANISM

Sus scrofa

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                                                                                                               Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(Attp://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 41 row: L column: 4
                 Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., ClRiggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
                                                                                                                                                                                                                        GSS; genome survey sequence. Tetraodon nigroviridis
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Class: BAC ends.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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Tetraodon nigroviridis DNA sequence
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/clone_lib="CHOR1-230 Segment 1"
/clone_lib="CHOR1-230 Segment 1"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SBNHed/MCW) BAC library produced by
Pieter de Jong"
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/mol_type="genomic מאס"
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/strain="BN/S8NH8d/MCW"
/db_xref="taxon:10116"
/clone="CH230-41L4"
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aodon nigroviridis, genomic survey
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Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis
Conome Res. 10 (7), 939-949 (2000)
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                                                            Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weisenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                           Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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Estimate of human ----
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GSS; genome survey sequence.
Tetraodon nigroviridis
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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1 (bases 1 to 438)

Ouellet, T., Dan, H., Koul, A., Chapados, J., Couroux, P.,
Harris, L.J., Hattori, J.I., Robert, L.S., Singh, J.A, Spr
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Ta01_AAPC ECORC Fusarium graminearum inoculated wheat heads
TritTcum aestivum cDNA clone Ta01_19e09, mRNA sequence.
BI751547
BI751547.1 GI:15773349
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Agriculture and Agri-food Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Ouellet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                         (613) 759-1658
(613) 759-1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                           ouellettr@agr.gc.ca.
Location/Qualifiers
              /note="Vector: pGEM-T easy; Site 1: EcoRI; Site 2: EcoRI; Controled chamber-grown wheat heads were spray inoculated at mid-anthesis with a Fusarium graminearum macroconidial suspension (50,000 spores/ml) and kept under intermitent
                                                                                               /dev_stage="anthesis"
/clone_lib="Ta01_AAFC_ECORC_Fusarium_graminearum_inoculate
d_wheat_heads"
misting for
                                                                                                                                                                                                                                   /organism="Triticum aestivum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="G"
/note="Genoscope sequence
end : T7"
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/mal_type="genomic DNA"
/db xref="taxon:99883"
/clone="075813"
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                                                                                                                                                       tissue_type="heads"
                                                                                                                                                                             /db_xref="taxon:4565"
/clone="Ta01_19e09"
                                                                                                                                                                                                                     cultivar="Frontana"
                                                                                                                                                                                                                                                                               .438
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  for 24 hours, then collected and
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Texas Children's Cancer Center and Human Genome Sequencing at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTGACCCCGCCCCTGGTCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F. Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM153575

499 bp mRNA linear EST 30-NOV-20
TCBAP2D9954 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP9954, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 832-824-4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.
1 (bases 1 to 499)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: clones@txccc.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 832-825-4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and Sall sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muzamatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
                                                                                                                                                                                                                           leukemTa Baylor-HGSC project=TCBA"

/note="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
/note="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
/rote strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGCGCAGGAGGAG(T)VN
3'; V=A,C,G; N=A,C,G;] and then dC tailed. Second strand
was primed with a BamHI-dC primer
[5'AGAGAGCTCGGGATCCGCGGCGCGCAATAATAATAAT(C) 3'].
                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="pediatric 2 years"
/lab_host="DH10B"
/clone_lib="Pediatric pre-B cell_acute lymphoblastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="leukopheresis"
/cell_type="pre-B cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="TCBAP9954"
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Pred. No. 3.4e+03;
1; Mismatches 1;
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Margolin, J.F.
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: leukemia
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Query Match Best Local Similarity

Conservative

85.0%; Score 17; DB 3; 100.0%; Pred. No. 3.4e+03 ive 0; Mismatches 0

Length 499;

Indels

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Gaps

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JOURNAL COMMENT
                                                                                 RESULT 13
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AUTHORS
TITLE
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Best Local Similarity
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CW754796 310 bp DNA linear OG BBa0057A15.r OG_BBa Oryza glaberrima genomic cl 3', genomic survey sequence.
CW754796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 214)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Christopher A. Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                         TTGACCCCGCCCCTGGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGACCCCGCCCCTGGT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                             /clone lib="NCI GAP GC6"
/rote="Vector: pT773D-Pac (Pharmacia) with a modified note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplied CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled germ
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:235544"
                                                                                                                                                                                                                                                                 84.0%;
                                                                                                                                                                                                                                                                 Score 16.8; DB 1;
Pred. No. 4.3e+03;
                                                                                                                                                                                                                                                 Mismatches
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                                            clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ph.D.,
                                       GSS 09-NOV-2004
one OG_BBa0057A15
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LOCUS
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AUTHORS
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JOURNAL
                                                                                                                                                                                                         AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TIGACCCCGCCCCTGGTCGT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sprinartoideae; Oryzeae; Oryza.

1 (Dases 1 to 310)

Kim,H., Yu,Y., Wissotski,M., Byrne,M., Stum,D., Smart,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                 A1882346 426 bp mRI
ub99b09.rl Soares_mammary_gland_NbMMG
IMAGE:1396601 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0057 row: A column: 15
Seg primer: CAC TCA TTA GGC ACC CCA
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Fax: 520 621 1259
Email: rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza glaberrima (African rice)
Oryza glaberrima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CW754796.1 GI:55593454
GSS.
    Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 411.
Location/Qualifiers
                                                                                                                                                                                                     1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2004)
                                                              MGI:908317
                                                                                   IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: TAA TAC GAC TCA CTA TAG
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/tissue type="young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OG_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza glaberrima"
/mol_type="genomic DNA"
/db_xref="taxon:4538"
/clone="OG_BBa0057A15"
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Pred. No. 4.2e+03;
D; Mismatches 2
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                                                                                     further information
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clone
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REFERENCE
AUTHORS
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VERSION
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BP640725/c
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                                                                                                                                                                                      Email: mseki@rtc.riken.go.jp
reversed clone; Please visit our web
(http://pfgweb.gsc.riken.go.jp/) for
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsis.

1 (Dases 1 to 434)

Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T., Nakajima,M., Enju,A., Akiyama,K., Oono,Y., Muramatsu,M., Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.

Functional annotation of a full-length Arabidopsis cDNA collection Science 296 (5565), 141-145 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Conservative
                                                                                                                                                                                                                                                                                               Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BP640725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP640725 RAFL19 Arabidopsis thaliana cDNA clone RAFL19-52-L12 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                           Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                     Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP640725.1 GI:49291977
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                     /tissue_type="mixture of silique and flower"
/lab host="DH10B"
/clone_lib="RAFF119"
                                                                                                       /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:1396601"
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/strain="C57BL/6J"
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note="Site_1: BamHI; Site_2: SalI; Subtraction Library"
                                                                                     clone="RAFL19-52-L12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="male"
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Pred. No. 4.2e+03;
0; Mismatches 2
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                                     Matches
                                             Query Match 84.0%;
Best Local Similarity 90.0%;
216
                                     18;
        1 TTGACCCCGCCCCTGGTCGT 20
TIGACCCCGCCCCTGCCCGT 197
                                     Conservative
                                     <u>,</u>
                                              Score 16.8; DB 3;
Pred. No. 4.2e+03;
                                      Mismatches
                                                        ω
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Search completed: April 10, 2006, 16:03:31 Job time: 1567.5 secs

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Run
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1: geneseqn1980
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Gapop 10.0 , Gapext 1.0
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Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	score	Query	Query Match Length DB	BB	ID
-	20	100.0	20	w	AAA07659
ი 2	16.8	84.0	1017	œ	ACA19614
C J	16.8	84.0	1026	11	ABD04465
C 4	16.8	84.0	1053	H	ABD04362
ъ	16.8	84.0	1617	11	ABD04301
6	16.4	82.0	890	13	ADX63316
7	16.4	82.0	1124	13	ADX49634
œ	16.4	82.0	1483	13	ADX46563
9	15.8	79.0	501	11	ABD04697
10	15.8	79.0	735	σ	ABN90562
c 11	15.8	79.0	819	Q	ABN90564
12	15.8	79.0	1008	4.	AAS54373
13	15.8	79.0	1020	11	ABD03622
14	15.8	79.0	1038	1	ABD03697
c 15	15.8	79.0	1221	11	ABD04007
c 16	15.8	79.0	1842	œ	ADA71243
17	15.8	79.0	1965	11	ABD04630
18	15.8	79.0	1980	w	AAZ51001
19	15.8	79.0	2000	0	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,

The invention relates to a HERG protein having a mutation compared to wild-type HERG, and is useful for developing products for the diagnosis, prevention and treatment of long QT (LQT) syndrome. The products and methods can be used for the diagnosis of bubjects with LQT syndrome. They can also be used to screen for drugs for treating or preventing LQT syndrome. The HERG nucleic acids can also be used for gene therapy and HERG peptides can be used for peptide therapy. Sequences AAAO7654-693

They

Claim 7; Page 72; 163pp; English.

New isolated mutant HERG nucleic acids, useful for developing products for the diagnosis, prevention and treatment of long QT syndrome.

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15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8
79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	•	79.0	79.0	79.0
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ADB53947	ADJ30693	ADA57676	ADD38113	ADC74644	ABX59943	ACC50893	ADA41545	AAL36955	ADJ30692	ADA57675	ADD38112	ADC74643	ABX59942	ACC50892	ADA41544	AAL36954	AAC75733	AAZ51000	ADV70146	ACN37667	ABZ34816	ADQ22316	ACC42478	ABD04809	AAS01678
Adb53947 CACNAIG g	Adj30693 Human mus	Ada57676 BAC fragm	Add38113 cDNA clon	Adc74644 Human sec	Abx59943 cDNA enco	Acc50893 Human sec	Ada41545 Human sec	Aal36955 Human mus	Adj30692 Human mus	Ada57675 BAC fragm	Add38112 cDNA clon	Adc74643 Human sec	Abx59942 cDNA enco	Acc50892 Human sec	Ada41544 Human sec	Aal36954 Human mus	Aac75733 Human ORF	Aaz51000 X. oryzae	Adv70146 Tumor-ass	Acn37667 Tumour-as	Abz34816 Coding se		Acc42478 Human C1Q	Abd04809 Pseudomon	Aas01678 Human T-t

ALIGNMENTS

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RESULT 1
AAAO7659
ID AAAO
XX AAAO
XX AAAO
XX HERG
XX HERG
XX PCR
XX PCR
XX POR
XX POR
XX POR
XX POR
XX IO-1
PF 20--
PF 20--
XX (UT)
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XX WPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keating MT, Splawski I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1998;
06-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reverse primer for amplifying HERG gene exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2000
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99US-00226012.
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RESULT 2
ACA19614/c
ID ACA19614 standard; DNA; 1017
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        The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid CC encoding a polypeptide whose expression is inhibited by the antisense CC nucleic acid; (2) a host cell expression is inhibited by the isolated CC polypeptide or its fragment whose expression is inhibited by the CC antisense nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC proliferation; (7) identifying a compound that influences the activity of CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an CC compound acts; (9) manufacturing an antibiotic; (10) profiling a gene
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                                                                    Claim 14; SEQ ID NO 7484; 1766pp; English.
                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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Trawick JD,
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overexpressed
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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or underexpressed;
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Pred. No. 16;
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Xu HH;
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RESULT 3
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Matches
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          prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in the print of the printed specification, but was obtained in
                                                                                                                                                  The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics,
                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial infection; gene; ds; Pseudomonas aeruginosa infection; antibacterial.
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                                                                                                                                                                                                                         Disclosure; SEQ ID NO 3069; 455pp; English.
                                                                                                                                                                                                                                                           pathological conditions resulting from bacterial infection.
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18; Conserv
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                                                  Nolling J,
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RESULT 4
ABD04362/c
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                                                                    polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biachting because of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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  Sequence
                                                    segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to Pseudomonas aeruginosa polypeptides and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rubenfield MJ,
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27-JUL-1998;
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98US-0094190P.
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  218 A;
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  338 C;
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Pred. No. 4.6e
0; Mismatches
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Query Match

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                                                                                                                            The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and cherapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a compound, such as a polypeptide, compound, such as compounds of compounds and cardy as targets for antibacterial darget, as targets for antibacterial darget, as targets for recombinant compounts for diagnosa derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa cardy as the components for diagnosis and/or treatment of P. aeruginosa sequences appoints for diagnosis and/or treatment of P. aeruginosa sequences ABD1197-cc ABD17967 represent P. aeruginosa polypucleotides of the invention. Note: The sequence data for this patent did not form part of the printed consortation but was obtained in electronic format from USPTO at
                               Matches
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                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 2905; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
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                                                                                                                     seqdata.uspto.
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                                             Local Similarity
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    TTGACCCCGCCCCTGGTCGT
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                                 Conservative
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                                                                                        B₽;
                                                                                                                     gov/sequence.html
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98US-0094190P.
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                                                                                        239 A;
                                             84.0%;
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                                                                                        555 C;
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                               Score 16.8; D
Pred. No. 4.6e
0; Mismatches
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                                             4.6e+02
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Query Match
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Matches 17
                                                                                                     plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cold tolerance; heat tolerance; drought tolerance; herbicide t extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance;
                                                                                                                                                                                                                                                                                                                           The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid available in electronic form from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             galactomannan production; lignin production; plant growth regulator;
yield; plant growth; plant development; seed oil; protein yield;
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                                                           Sequence 890
                                                                                                                                                                                                                                                                                              of the invention are also useful in physical arrays of molecules and as
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 34159; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-180133/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-2001; 2001US-00985678
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              Local Similarity
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n content; gene; ss.
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KOVALIC D K.
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                                                           C; 256 G;
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Pred. No. 7e+02;
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                                                           219 T; 0 U; 0 Other;
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tolerance; herbicide tolerance;
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                                                                 The invention describes a recombinant DNA construct comprising a colymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at fip. seqdata.uspto.gov/sequence.html?DocID:2004034883. The polynucleotide of the invention are also useful in physical arrays of molecules and as comproving plant tolerance to cold, heat, drought, herbicides, extreme common conditions, pathogens or pests, for manipulating growth rate in colls by modification of the cell cycle pathway, for conferring conditions, pathogens or pests, for manipulating growth rate in colls by modification of the cell cycle pathway, for conferring conferring increased resistance to plant disease, for producing galactomannan, conferring conferring increased resistance to plant disease, for producing galactomannan, compant or plants, for improving yield by modification of plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrates, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrates, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrates, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrates, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrates, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrates, nitrogen or phosphorus use and/or uptake corbitosynthesis or carbohydrates, nitrogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
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05-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 24374; 15pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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Sequence 1124 BP;

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Length 1124;

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The invention describes a recombinant DNA construct comprising a conjunct polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at fip.seqdata.uspto.gov/sequence.html?DocID:200403488. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, cc lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of conformation in plants, for improving yield by modification of uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                           New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (/noHZ)
                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 21303; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                            Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1999;
05-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant full length insert polynucleotide seqid 21303.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KOVA/)
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SCREEN S E.
TABASKA J E.
CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACCCCGCCCCTGGTCG
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                                                                                                                                                                                                                                                                                               yield.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00304517
2001US-00985678
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                                                                                                                                                                                                                                                                                                                                                                                                            Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                            Screen SE, Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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RESULT 9
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                                                                           The invention relates to Pseudomonas aeruginosa polypeptides and the CC polymucleotides encoding them. The sequences are useful in diagnosis and CC therapy of pathological conditions, as molecular targets for diagnostics, CC prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, CC for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, cc including anti-P. aeruginosa drugs, as templates for recombinant CC production of P. aeruginosa drugs, as templates for recombinant CC components for diagnosis and/or treatment of P. aeruginosa-clerived peptides or polypeptides, as target CC of Pseudomonas species using biochip technology. Sequences ABD1397-CC ABD17967 represent P. aeruginosa polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct invention.
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                                                    specification but was obtained seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3301; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathological conditions resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa polynucleotide #3301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-615309/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nolling J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΒP
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from bacterial infection.
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Best Local Similarity

79.0%;

Score 15.8; Pred. No. 1

8; DB 11; 1.3e+03;

Length 501;

Query Match

Sequence

501

BP;

77

A; 177 C; 160 G;

87 T;

0 U; 0 Other;

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RESULT 11
ABN90564/c
ID ABN90564 standard; D:
XX
AC ABN90564;
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Best Local
                                                                                                                                                                                                                                                           ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus antibacterial;
                                                                                                                                                                                                                                       Sequence 735 BP; 121 A; 250 C; 237 G; 127 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 25; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN90562 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-)
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                                                                                                                                         221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                       l Similarity
17; Conserv
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                                                                                                                                           TTGACCCCCCCCTTGGCCG
                                                                                                                                                                  TTGACCCCGCCCCTGGTCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGACCCCGCCCCTGGTCGT
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                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THERAPEUTICS CORP.
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97US-0064964P.
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                                                                               DNA;
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                                                                                                                                                                                                     Score 15.8;
Pred. No. 1.
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RESULT 12
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequence given in ABP35124 to ABP37960. The S. epidermidis sequences have
21-MAR-2000;
23-MAY-2000;
                                                                                                                                                  Antisense; ds; prokaryotic cellular proliferation antibacterial; drug design.
                                                                                                                                                                                                                                                                               AAS54373 standard; DNA; 1008 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 819 BP; 144 A; 261 C; 274 G; 140 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 27; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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08-NOV-1997;
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                                        21-MAR-2001;
                                                                     27-SEP-2001
                                                                                                                          Pseudomonas aeruginosa.
                                                                                                                                                                                            Pseudomonas aeruginosa DNA for cellular proliferation protein #504.
                                                                                                                                                                                                                         13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                               TTGACCCCGCCCCTGGTCG 19
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                        2001WO-US009180
2000US-0191078P.
2000US-0206848P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epidermidis; open reading frame; \mathsf{ORF}_i bacterial infection; gene therapy; gene; ds.
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97US-0064964P.
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                                                                                                                                                                                                                                                                                                                                                                                                                        79.0%;
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Pred. No. 1.3e+03;
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RESULT 13
ABD03622
ID ABD03
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AC ABD03
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DT 29-J1
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PBeux
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli, Staphylococcus aureus, Salmonella typhi, Klabsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antiblotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential professories
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23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia
                               18-FEB-1998;
27-JUL-1998;
                                                                                                              18-FEB-1999;
                                                                                                                                                                                                                               US6551795-B1
                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                        antibacterial
                                                                                                                                                                                                                                                                                                                                                            Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa polynucleotide #2226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABD03622 standard; DNA; 1020 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this pat did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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Yamamoto RT,
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17; Conserv
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; 2000US-0242578P.
; 2000US-0253625P.
; 2000US-0257931P.
; 2001US-0269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Xu HH;
                               98US-0074788P.
98US-0094190P.
                                                                                                                 99US-00252991
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1008;
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RESULT 14
ABD03697
ID ABD03697
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
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                                                                                    WPI; 2003-615309/58.
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27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa polynucleotide #2301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment o
                                                                                                                                                                                                      (GENO-) GENOME
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98US-0094190P.
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Pred. No. 1.
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Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

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P-PSDB;
  The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics
                                                                                                                            Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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                                                                                                                                                                                                                                                                               Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1999;
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                                                                                     Disclosure; SEQ ID NO 2611; 455pp; English
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27-JUL-1998;
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DB; ABO70436.
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98US-0094190P.
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                                                                                                                                                            Sequence 1221 BP; 210 A; 353 C; 437 G;
                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html
                                                                                                 Local
186 TTGACCCTGGCCCTGGTCG
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AC140158 Felis cat
AC15521 Felis cat
AC157414 Bos tauru
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AC128637 Rattus no	AC090316 Homo sapi		AC162724 Papio anu	AP001558 Homo sapi	AP000928 Homo sapi	AP001187 Homo sapi	AP003293 Oryza sat	BX927084 Danio rer	AP003221 Oryza sat	AC116426 Genomic 8	BX276127 Zebrafish	AP000814 Homo sapi	AC105931 Magnaport	Continuation (52 o	Continuation (340	Continuation (4 of	CP000089 Dechlorom	AC000159 Homo sapi	AC119405 Magnaport	AC006966 Homo sapi	AE004540 Pseudomon	L43507 Pseudomonas	AJ844252 Tarphius	AJ844251 Tarphius	AJ844250 Tarphius	AJ844248 Tarphius	

ALIGNMENTS

ACCESSION VERSION KEYWORDS AR139544
LOCUS
DEFINITION
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VERSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 2 BD223633 LOCUS REFERENCE AUTHORS TITLE JOURNAL FEATURES 닭 δ ORIGIN SOURCE DEFINITION Best Loc Matches Query Match Best Local Similarity ORGANISM gene. BD223633 BD23633.1 GI:33033403 JP 2002521065-A/59. Unclassified.
1 (bases 1 to 20)
1 (bases 1 to 20)
Keating,M.T. and Splawski,I.
Mutations in and genomic structure of HERG--a long QT syndrome Patent: US 6207383-A 61 27-MAR-2001;
Location/Qualifiers Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; 20; Sequence AR139544 Mutations Homo sapiens (human) Unknown. Unknown AR139544.1 TTGACCCCGCCCTGGTCGT 20 100.0%; Score 20; DB 6; ilarity 100.0%; Pred. No. 3.4e+02; Conservative 0; Mismatches 0; 61 from /organism="unknown" /mol_type="unassigned in and GI:14482040 genomic patent SD structure 20 bp S 6207383. of DNA DNA A linear HERG - a lon Length 20; linear long PAT PAT 17-JUL-2003 QT syndrome 0; Gaps gene 0

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C12N5/10,C12N5/10,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/ PC
C12N5/00,C12N5/00,C12N5/00
CC Mutations in and genomic structure of HERG - a long QT CC
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Patent: JP 2002521065-A 59 16-JUL-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION
OS Homo sapiens (human)
PN JP 2002521065-A/59
PN JF 2002521065-A/59
PP 16-JUL-2002
PP 20-JUL-1999 JP 2000562554
PF 27-JUL-1999 JP 2000562554
PR 27-JUL-1998 US 09/122847,06-JAN-1999 US 09/226012 PI
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C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15,C12N1/19,
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                                                                                                                                                                                            Patent: EP 1553190-A 61 13-JUL-2005;
The University of Utah Research Foun
Location/Qualifiers
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Mutations in and genomic structure of
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
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                                                                                 Score 20; DB 6;
Pred. No. 3.4e+02;
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TITLE
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RS Hillier,L.W., Fulton,R.S., Fulton,L.A., Graves,T.A., Pepin,K.H., Wagner-McPherson,C., Layman,D., Maas,J., Jaeger,S., Walker,R., Wylie,K., Sekhon,M., Becker,M.C., O'Laughlin,M.D., Schaller,M.E., Fewell,G.A., Delehaunty,K.D., Miner,T.L., Naah,W.E., Cordes,M., Du,H., Sun,H., Edwards,J., Bradshaw-Cordum,H., Ali,J., Andrews,S., Isak,A., Vanbrunt,A., Nguyen,C., Du,F., Lamar,B., Courtney,L., Kalicki,J., Ozersky,P., Bielicki,L., Scott,K., Holmes,A., Harkins,R., Harris,A., Strong,C.M., Hou,S., Tomlinson,C., Daughin-Kohlberg,S., Kozlowicz-Reilly,A., Leonard,S., Rohlfing,T., Strowmatt,C., Latreille,P., Miller,N., Johnson,D., Murray,J., Strowmatt,C., Latreille,P., Miller,N., Johnson,D., Murray,J., Woessner,J.P., Wendlam,A.M., Abbott,A., Minx,P., Maupin,R., Spieth,J., Bieri,T.A., Nelson,J.O., Brontowicz,N., Wohldmann,P.E., Cook,L.L., Hickenbotham,M.T., Eldred,J., Williams,D., Bedell,J.A., Mardis,E.R., Clifton,S.W., Chissoe,S.L., Marra,M.A., Raymond,C., Mardis,E.R., Cilfton,S.W., Chissoe,S.L., Marra,M.A., Raymond,C., Bubb,K., Simms,E., Levy,R., Clendenning,J., Kaul,R., Kent,W.J., Furey,T.S., Baertsch,R.A., Berent,M.R., Keibber,E., Flicek,P., Bork,P., Suyama,M., Bailey,J.A., Portnoy,M.E., Torrents,D., Chiswalla,A.T., Gish,W.R., Kedberson,J.D., Olson,M.V., Eichler,E.E., Green,E.D., Waterston,R.H. and Wilson,R.K.

Eichler, E.E., Green,E.D., Waterston,R.H. and Wilson,R.K.
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Direct Submission
Submitted (10-MAY-2000) Genome Se
University School of Medicine, 44
MO 63108, USA
6 (bases 1 to 16879)
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Waterston, R.H.
Direct Submission
Submitted (04-0CT-1999) Genome Submitt
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Direct Submission

Submitted (03-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.

MO 63108, USA
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Harkins,R., Lamar,B. and Stonekins,T.
The sequence of Homo sapiens BAC clone RP11-166D23
Unpublished (2001)
                              Direct Submission
Submitted (30-SEP-2000)
                                                                                                                                                                                                                                                                                   Submitted (12-JUN-2000)
University School of Med
                                                                                                                                                                                                                                                                                                                                                                                                                               6 (bases 1 to 16879)
Waterston, R.H.
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7 (bases
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Mammalia; Eutheria;
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RP11-166D23
Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
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4444 Forest to 16879)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (31-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On May 3, 2000 this sequence version replaced gi:6007897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The clone sequenced to the left is RP11-148K1 the clone sequenced to the right is RP4-548K24, 200 base pair overlap. Actual end of this clone is at base position 77856 of RP4-548K24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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Direct Submission
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1018. .1075
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/db_xref="taxon:9606"
/chromosome="7"
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                                                                                                                                                       rpt_family="L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .16879
                                                                                          _family="MIR"
                                   family="CT-rich"
                                                                   .1874
                                                                                                                                                                                                                                                                                                                                                                                                           _lib="RPCI-11"
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RESULT 5 AC146440

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DEFINITION
ACCESSION

Pan troglodytes AC146440

181369 bp DN BAC clone RP43-11P11

DNA 1:

linear

PRI 18-AUG-2004

complete sequence.

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8622 TTGACCCCGCCCCTGGTCGT 8603
                                                              20;
                                                                               Similarity
                 TTGACCCCGCCCCTGGTCGT 20
                                                            100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                              /rpt_family="L2" 9793. .10006
                                                                                                                                                                                                                                                                                                     H_NH0166D23.1.2
This gene was based on gi(12804922)
Continues as H_DJ0548K24.1.2"
                                                                                                                                                                                                                                                                                                                                                                /note="Homo sapiens, Similar to potassium voltage-gated channel, subfamily H (eag-related), member 2, clone MGC:3324 IMAGE:3510423, mRNA, complete cds.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="MIR" 8007. .8778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8449. .>8578
/gene="KCNH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H NH0166D23.1.1
                                                                                                                           rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="CpG island (%GC=74.0, o/e=0.78, #CpGs=87)"
3113. .8165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAS07566.1"
/protein_id="AAS07566.1"
/db_xref="GI:41474663"
/rtanslation="MPVRRCHVAPQNTFLDTIIRKFEGQSRKFIIANARVENCAVIYC
NDGFCELCGYSRAEVMQRPCTCDFLHGPRTQRRAAAQIAQALLGAEERKVEIAFYRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Continues as H_DJ0548K24.1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This gene was based on gi(4557728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Homo sapiens potassium voltage-gated channel,
subfamily H (eag-related), member 2 (KCNH2), mRNA.;
                                                                                                                                                                                         rpt_family="G-rich"
                                                                                                                                                                                                                                                 protein_id="AAS07567.1"
/db_xref="GI:41474664"
                                                                                                                                                                                                                                                                                  product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="(GGGGA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="unknown"
                                                                                                                                                                                                                               translation="MQRPCTCDFLHGPRTQRRAAAQIAQALLGAEERKVEIAFYRKD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="KCNH2"
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                                                                                                                                                                                                                   .8680
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                                                            0;
                                                                              Score 20; DB 8; 1
Pred. No. 1.4e+02;
                                                                Mismatches
                                                                                             Length 16879;
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                                                                         source
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Direct Submission

Submitted (18-AUG-2004) Washington University School of Medicine,
Submitted (18-AUG-2004) Washington University School of Medicine,
MO
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Submitted (27-APR-2004) Genetics, Genome Sequencing Submitted (27-APR-2004) Senetics, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63108, USA
On Jul 10, 2004 this sequence version replaced gi:46576152
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Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 181369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 181369)
Shah, N. and Bielicki, L.
The sequence of Pan troglodytes BAC unpublished (2001)
                                                                                                                        This
                                                                                                                                                                                                            The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #C0471, birthdate: 6-6-80). The clone and detailed information can be obtained from ResGen (http://www.resgen.com) or Pieter de Jong and co-workers at
                                                                                                                                                                                                                                                                                                                                                                              Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, sethtp://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-JUL-2004) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson, R.K.
Direct Submission
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4 (bases 1 to 181369)
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HTG.
                                                                                                                                         NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                           http://www.bacpac.chori.org.
                                                                                                                                                                                                                                                                                                                                     SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: C_PT011P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                      sequence is the entire insert
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                Location/
                                                                       .181369
                                                                                             Qualifiers
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                               * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Sep 6, 2001 this sequence version replaced gi:14626400.
                                                                                                                                                                                                                    Sequencing vector: plasmid; 97% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 97% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 151018 bases at least Q40 Consensus quality: 160531 bases at least Q30 Consensus quality: 160531 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.

1 (bases 1 to 216408)
Waterston, R.H.
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Homo sapiens chromosome UNK clone RP11-606P1, WORKING DRAFT
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: H_NH0606P01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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95997. 97195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Unresolved tandem repeat."
101465. .101541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP43-11P11"
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10000: contig of 10000 bp in 10100: gap of unknown length
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Pred. No.
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AUTHORS
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HSA010538/c
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                                                       Direct Submission
Submitted (20-AUG-1998) Armstrong M.J., Function
Janssen Research Foundation, 30 Turnhoutseweg,
Location/Qualifiers
                                                                                                                                                                      Armstrong, M.

Analysis of the human HERG gene: intron localisation and identification of a novel inherited mutation associated with long
                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                 cardiac specific; ether-a-go-go-related protein; herg gene;
potassium channel.
                                                                                                                 2 (bases 1 to 331)
Armstrong, M.J.
                                                                                                                                                                                                               Yang, P., Paulussen, A.,
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AJ010538.1 GI:3452412
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  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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13261. .38907
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13161. .13260
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11589. .11688
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38908. .39007
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|1689. .13160
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'chromosome="UNK"
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|mol_type="genomic DNA"
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11688: gap of unknown length
13160: contig of 1472 bp in length
13260: gap of unknown length length
38907: contig of 25647 bp in length
39007: gap of unknown length
216408: contig of 177401 bp in length
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BA000030_06
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BA000030_09
BA000030_11
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PGOLPSPRAHSLNIPDASGSSCSLARTRSRESCASVRRASSADDI EAMRAGVLPPPRH
ASTGAMHPLRSGLLNSTSNSDLVRYETI SKI PQITILMEVDLKGDPFLASPTSDREI I A
PKI KERTHNVTEKVTQVLSLGADVLPEYKLQAPRI HRWT I LHYS PFKAVWDWLI LLLV
I YTAVFTEYSAAFILKETEEGPPATECGYACQPLAVVDLI VDIMFI VDI MI INFRTTYV
NANEEVVSHPGRI AVHYFKGWFLI DWYAA I PPDLLI FGSGSEELI GLLKTARLLRLVR
VARKLDRYSEYGAAVLFLLMCTFALI AHWLACI WYA I GMMEQPHMDSR I GWLHNLGDQ
I GKPYNGSGLGGPSI KOKYVTALYFTFSSLTSVGFGNVSPNTNSEKI FSI CVMLI GSL
MYAASI FGNVSAI I QRLYSGTARYHTQMLRVREPI RFHQI PNPLRQRLEEYFQHAWSYT
NGI DMNAVLKGFPECLQADI CLHLNRSILLQHCKFPRGATKGCLLALAMKFKTTTHAPPG
DTILVHAGDLLTALYFI SRGSI EI LRODVVAA I LGKNDI FGSPLMLYARPGKSNGDVRA
LTVCDLHKLHRDLLEVLDMYPEFSDHFWSSLEI TFNLRDTMI PGSPGSTELEGGFS
RGRKRKLSFRRRTDKDTEDPGESVSALGPGRAGAGFSSRGRPGGDWGSSPSSGESSESS
SEDEGFGRSSSPLRLVPFSSPRPFGEPPGGBPLMEDCEKSSDTCNPLSGAFSGVSNIF
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GPRTQRRAAAQIAQALLGAEERKVEIAFYRKDGSCFLCLVDVVPVKNEDGAVIMFILN
FEVVMEKDMVGSPAHDTNHRGPPTSWLAPGRAKTFRLKLPALLALTARESSVRSGGAG
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join(5]. 281,AJ010539.1:51. 215,AJ010540.1:51. .494,
AJ010541.1:51. 262,AJ010542.1:51. .479,AJ010543.1:51.
AJ010544.1:51. 250,AJ010545.1:51. .303,AJ010546.1:51.
AJ010547.1:51. .150,AJ010548.1:51. .323,AJ010549.1:51.
AJ010550.1:51. .227,AJ010551.1:51. .200)
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/number=2
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/protein id="CAA09232.1"
/db xref="G1:3452413"
/db xref="GOA:012809"
/db xref="UniProt/Swiss-Prot:Q12809"
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function="cardiac specific potassium channel"
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AC150790 1/c
WPCOMMENT
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VERSION
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AC140158/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pieces.
AC140158
                  Submitted (22-FEB-2003) NIH Intramural Sequencing Center, Grovement Circle, Gaithersburg, MD 20877, USA 3 (Dases 1 to 155060) Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
Felinae; Felis.
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HTG; HTGS PHASE2; HTGS DRAFT.
Felis catus (cat)
Felis catus
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Akhter, N., Antonellis, A.,
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RP86-578M14,
                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Laurasiatheria; Carnivora; Fissipedia; Felidae;
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Pred. No. 1.5e+03;
0; Mismatches 1
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Gaps

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clone

CH240-469N

G 03-APR-2003 18 ordered

BA000030_45 BA000030_46 BA000030_47

BA000030_49 BA000030_41 BA000030_42 BA000030_43 BA000030_43 BA000030_44

BA000030_37 BA000030_38 BA000030_39

BA000030_32 BA000030_33 BA000030_34 BA000030_35 BA000030_36

BA000030_30 BA000030_30 BA000030_31 BA000030_32

BA000030-24
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COMMENT
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                                                                                                                                                                                                                                                        consists of 18 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

8364
8463: gap of unknown length
12801: contig of 8363 bp in length
12802: loontig of 4338 bp in length
12802: contig of 4338 bp in length
12504: loontig of 4338 bp in length
12504: contig of 4338 bp in length
12504: contig of 1262 bp in length
25925: 38785: contig of 12661 bp in length
25925: 38785: contig of 12661 bp in length
25926: gap of unknown length
25928: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently
  8364
8462
12802
112902
112902
115264
115264
115268
25825
25825
28886
38886
38886
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Consensus quality: 152104 bases at least Q40
Consensus quality: 152758 bases at least Q30
Consensus quality: 153143 bases at least Q20
Consensus quality: 153143 bases at least Q20
Insert size: 160000; agarose-fp
Insert size: 15380; sum-of-contigs
Quality coverage: 11.84x in Q20 bases; sum-of-contigs
Quality coverage: 12.36x in Q20 bases; sum-of-contigs
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Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: dzg
Center clone name: 578M14
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101800:

    Summary Statistics

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of unknown length
g of 20393 bp in length
of unknown length
ug of 6788 bp in length
of unknown length
of unknown length
g of 6467 bp in length
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of 2534
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bp in length
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126003
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.08689. .108788
----ated length=unknown
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50889. .50988
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AC135221 clone RP86-367F9 (center project name dzf)
                                           note="assembly_fragment"
117890. .117989
estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment"
[01801. .101900
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note="assembly_fragment"
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75422. .81307
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note="assembly_fragment"
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'clone="RP86-578M14"
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Chu, G., Coleman, B., Coleman, C., Hu, P., Laric, P., Lee-Lin, S.-Q., Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                         Submitted (21-MAY-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On May 21, 2003 this sequence version replaced gi:28467152.
                                                                                                                                                                                                                                                                                                                                            Submitted (09-OCT-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 156383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC135221
AC135221.3 GI:30962732
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC135221 156383 bp DNA linear H' Felis catus clone RP86-367F9, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TGACCCCGCCCCTGGTCGT 20
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis
                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                       Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 156383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 156383)
                        Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
._____ project Information
                                                                                 Center: NIH Intramural Sequencing Center code: NISC
Web site: http://www.nisc.nih.gov
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Center project
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vector_side:right"
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144417. .155060
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122776. .12
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44317. .144416
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|41651. .144316
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41551. .141650
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94.7%;
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                                                                                                                                                Center
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E, 13 ordered
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                              gap
                                                                                                                                             misc_feature
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Consensus quality: 154058 bases at least Q40
Consensus quality: 154058 bases at least Q30
Consensus quality: 154051 bases at least Q30
Consensus quality: 155011 bases at least Q20
Insert size: 155103; sum-of-contigs
Quality coverage: 11.75x in Q20 bases; sum-of-contil
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Center clone name: 367F09

The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a phase deep trimmed away, and each base is associated with a phase deep trimmed away, and each base is associated with a phase deep trimmed away. with a Phrap-derived quality score. --- Summary Statistics the indicated

agarose-fp sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence as soon as it is available and the accession 106624 126321 126421 141406 141506 146217 103530 103630 106524 100102 clone_end:T7
vector_side:left"
273. .372 organism="Felis catus" note="assembly_fragment clone_ db_xref="taxon:9685" clone="RP86-367F9" ocation/Qualifiers ion number will be preserved.

272: contig of 272 bp in length

372: gap of unknown length

3968: contig of 3596 bp in length

4068: gap of unknown length

6730: contig of 2662 bp in length

6830: gap of unknown length

6830: gap of unknown length

35503: contig of 28673 bp in length

35603: gap of unknown length

75477: contig of 3874 bp in length type="genomic 75577 9: gap of unknown length
3: contig of 2894 bp in length
3: gap of unknown length
0: contig of 19697 bp in length
0: gap of unknown length
5: contig of 14985 bp in length
6: gap of unknown length
6: contig of 4711 bp in length
6: gap of unknown length gap of contig gap of contig gap of contig gap of gap of unknown leng gap of unknown length contig of 3328 bp in length f unknown length g of 8256 bp in length f unknown length g of 16168 bp in length in length

REFERENCE AUTHORS

JOURNAL

TITLE JOURNAL

estimated_length=unknown

JOURNAL REFERENCE AUTHORS TITLE

TITLE

REFERENCE AUTHORS

ACCESSION VERSION

KEYWORDS

AC135221/c LOCUS

DEFINITION

SOURCE ORGANISM

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Matches

18;

gap

misc_feature

misc_feature

gap

misc_feature

gap

misc_feature

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RESULT 12
AC157414/c
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KEYWORDS
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Best Local
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                                                                                                                                                                                        47216 TGACCCCGCCCTGCTCGT 47198
                            Bos taurus clone CH240-66017, *** SEQUENCING IN PROGRESS unordered pieces.
AC157414
AC157414 BC1:68302799
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Bos taurus (cow)
                                                                                                                                                                                                                  2 TGACCCCGCCCCTGGTCGT 20
                Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                           Bos taurus (cow)
                                                                                                                                                                                                                                                              Similarity
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146317. .156383
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106624. .126320
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83834. .83933
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75578. .83833
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
141406. .141505
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103530. .103629
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75478. .75577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="clone overlaps with AC140158 clone RP86-578M14
                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                        estimated_length=unknown/
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.6730
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Pred. No. 1.5e+03;
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Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eggan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Poster, M., Gebregorgis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Gurra, M., Gurrathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harnes, S., Hladun, S.L., Hodgson, A., Hogues, M., Hernandez, J., Haels, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, L., Louise, S., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Louise, Edd, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Martin, R., Morris, S., Montemayor, J., Moore, S., Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Rives, C., Rodey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Shetty, J., Sheard, S., Song, X., Z., Socelle, R., Soes, J., Sands, D., Shety, J., Shery, S., Song, X., Z., Socelle, R., Soes, J., Wallsan, D., Walton, L., Walter, B., Wang, J., Walter, B., Wang, J., Walter, B., Wang, J., Walter, R., Walter, R., Walter, B., Wang, J., Walter, R., Walter, R., Walter, B., Wang, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Wrish, R., Walter, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinster, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinster, R., Smith, D.R., Holt, R.A., Smith, H.O., Weins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cardenas, V., Carter, K., Cavazos, I., Leausa, I., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L., Claveland, C., Cockrell, R., Cox, C., Coyle, M., C., Dederich, D., Davila, M.L., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davy-Carroll, L., De Anda, C., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Denson, S., Deramo, C., Delgado, O., Delgado, O., Denson, S., Deramo, C., Delgado, O., Denson, S., Deramo, C., Delgado, O., Delgado, O., Denson, S., Deramo, C., Delgado, O., Delgado, 
                                                                           Submitted (01-JUI-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 29, 2005 this sequence version replaced gi:59858648. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-PEB-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 212682)
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by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Muzny, D., Metzker, M., Adams, C., Agbai II, O., Allen, C., Muzny, D., Metzker, M., Ardams, C., Agbai II, O., Allen, C., Bangura, L., Alsbrooks, S., Archer, P., Arredondo, H., Bandaranaike, D., Bangura, L., Beltran, B., Beltran, R., Beraducci, A., Biswalo, K., Blyth, P., Bonham, H., Buhay, C., Burch, P., Cadoree, I., Canada, A., Cardenas, V.,
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mol_type="genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17870. .118409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   escimated length=293
15310. .115727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        estimated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      estimated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     estimated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       estimated
                                                                                                                                                                                                                                                                                                                                            218381
clone CH240-115C4,
                                                                                                                                                                                                                            (COW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lone="CH240-66017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _xref="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211652: gap of unknown
212682: contig of 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .157015
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                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _length=550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _length=154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length=183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _length=50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.4; DB 1
Pred. No. 1.4e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                              . bp DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14;
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bp in length
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE,
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E, 4 ordered
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Dingy C. Dinh, H. Donlin, J. McCauley, S. Dugan-Rocha, S. Dunn, A. Diuda, D., Egan, A., Escotto, M., Espinosa, V., Eugene, C., Fra, M., Pernandez, S., Fernando, P., Flagg, N., Forbes, L., Foster, P., Fowler, G., Fu, Q., Fuh, E., Garcia, A., Garcia, R., Garzer, D., Gaskin, C., Gench, S., Ghose, S., Gill, R., Gonzalez, D., Gonzalez-Garay, M., Guevara, W., Holder, M., Haaland, W., Haeberlen, K., Hawes, A., Hawdin, B.E., Hayes, S., Hemphill, L., Hernandez, J., Hines, S., Hitchens, M., Hodgson, A., Hogues, M., Hollins, B., Hayes, S., Hemphill, L., Hernandez, J., Jackson, L., Jiang, H., Johnson, B., Johnson, R., Kalafus, K., Kelly, S., Keys, T., Khan, Z., King, L., Kovar, C., Kowis, A., Kowis, C., Lara, F., Leal, S., Lee, K., Lee, S., LeGall, F.I., Lemon, S., Lewis, L., Li, B., Li, Y., Li, Z., Linnell, M., Holly, K., Manbouri, D., Martinez, E., Maleshwari, M., Mahoney, C., Malloy, K., Manbouri, D., Martinez, E., Minja, E., Morgan, M., Morris, S., Munidasa, M., Murray, D., Mazarith, L., Ngo, D., Nguyen, N., Norwig-Eastaugh, E., Nott, A., Nazarith, L., Ngo, D., Nguyen, N., Norwig-Eastaugh, E., Nott, A., Nazarith, L., Ngo, D., Nguyen, N., Norwig-Eastaugh, E., Nott, A., Nazarith, L., Ngo, D., Petrosino, J., Pham, T., Primus, E., Put, L., Perez, A., Perez, L., Petrosino, J., Pham, T., Primus, E., Put, L., Perez, A., Perez, L., Sana, M., Sanders, W., Santibanez, J., Santos, R., Sorelle, R., Svatek, A., Taylor, E., Song, X.-Z., Sorelle, R., Svatek, A., Taylor, T., Thomas, M., Thorn, R., Thornton, R., Trejos, Z., Usmani, K., Wheeler, D., Walliams, G., Williams, G., Walliams, R., Warten, J., Wall, R., Wu, J., Yu, F., Zhang, J., Zhang, Z., Direct, Submission, G., Mang, J., Kang, J., Zhang, Z., Direct, Submission, G., Walliams, R., Walliams, R., Wu, J., Zhang, Z., Direct, Submission, G., Walliams, R., Marten, J., Wall, R., Wu, J., Yu, F., Zhang, J., Zhang, Z., Leans, J., Santos, R., Santos, R., Santos, R., Santos, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-AUG-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Aug 20, 2004 this sequence version replaced gi:50726741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (27-JUL-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carter, K., Cavazos, I., Chacko, J., Chahrour, M., Chavez, D., Chen, G., Chen, R., Cheng, M.-T., Chu, J., Clerc, K., Cockrell, Coyle, M., Cree, A., Curry, S., Dai, W., Davila, M.L., Davis, C. Davy-Carroll, L., De Anda, C., Delgado, O., Denson, S., Deramc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inpublished
                                  (bases 1 to 218381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 218381)
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: FERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavazos, I., Chacko, J., Chahrour, M., Chavez, D., Chen, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chu, J., Clerc, K., Cockrell, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deramo, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department
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FEATURES

Location/Qualifiers

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 37410 contig of 37410 bp in length

* 37411 37910: gap of 500 bp

* 37911 167201: contig of 129291 bp in length

* 167202 167551: gap of 350 bp

* 167552 187482: gap of 19731 bp in length

* 187483 187482: gap of 200 bp

* 187483 218381: contig of 30899 bp in length.

of a Phase 2 submission. The indicated order and orientation of each sequence has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between them are based on estimates that have of the gaps between them are based on estimates that have

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clone="CH240-115C4"

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

JOURNAL

REFERENCE AUTHORS TITLE

JOURNAL

ORIGIN

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187483 . 218381
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misc_feature misc_feature

/estimated_length=500 37911. .167201

/note="assembly_name:Contig23" 167202. .167551

note="assembly_name:gap"

.167551

Matches

18;

Conservative

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Mismatches

Gaps

0

Query Match Best Local Similarity

87.0%; 94.7%;

Score 17.4; DB 14; Length 218381; Pred. No. 1.4e+03;

COMMENT

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* The sequence data in this record represents an 'enhanced' version

RESULT 14 AC098101/c LOCUS SOURCE ORGANISM REFERENCE DEFINITION 밁 KEYWORDS VERSION ACCESSION AUTHORS 112566 TGACCCCGCCCCTGGTCCT 112548 2 TGACCCCGCCCCTGGTCGT 20 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 243300) HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
Rattus norvegicus Rattus norvegicus clone CH230-82P23, WORKING DRAFT SEQUENCE, Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., AC098101.6 GI:30520383 AC09810: unordered pieces. AC098101 243300 bp DNA linear HTG 10-MAY-2003

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Allen, C., Allen, H., Alsbrocks, S., Amin, A., Anguiano, D.,
Anyabeechi, V., Aoyaeji, A., Ayodeji, M., Baca, B., Baden, H.,
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Rigs, F., Polindexter, A., D
                         Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:22855423.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 243300)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 243300)
reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
AC150514
                                                                                                                                                                         SOURCE
ORGANISM
                                                                                                                                                                                                                                              VERSION
KEYWORDS
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                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           POCUS
                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
Matches
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

TITLE

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pieces.
AC150514
AC150514.
AC150514.6 GI:51468284
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
BOB_taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shotgun sequence only contigs will be indicated in the feature table.
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                    Bos taurus
                                                                                                                                                                                                                                  Bos taurus
               Pecora; Bovidae; Bovin
1 (bases 1 to 236115)
                                                                                                                                                                                                                                                   AC150514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                            TTGACCCCGTCCCTGGTCG 152369
                                                                                                                                                                                                                                                                                                                                                                                                      TTGACCCCGCCCCTGGTCG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor Co
Center code: BCM
Web site: http://
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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236801. .240318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172928. .174668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /eBtimated_length=unknown
241640. .241739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="wgs_contig"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="CH230-82P23"
                                                                                                                                                                                                                             236115 bp DNA linear HTV clone CH240-109B14, WORKING DRAFT SEQUENCE,
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                                   Bovinae; Bos.
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Adams, C.,
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Chen, G., Chen, R., Cheng, M.-T., Chu, J., Clerc, K., Cocketell, R., Coyle, M., Cree, A., Curry, S., Dal, W., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Donlin, J., McCauley, S., Dugan-Rocha, S., Dunn, A., Durbin, K., Driuda, D., Egan, A., Escotto, M., Espinosa, V., Engene, C., Fa, M., Fernandez, S., Fernando, P., Flagg, M., Forbes, L., Foster, P., Gaskin, C., Gench, S., Ghose, S., Gill, R., Garcia, R., Garner, T., Gaskin, C., Gench, S., Ghose, S., Gill, A., Garcia, R., Garner, T., Gonzalez, Gary, M., Guevara, W., Holder, M., Harbes, R., Havlak, P., Hall, B., Hamid, H., Hamilton, K., Harbes, B., Harris, R., Havlak, P., Hawes, A., Hawkins, E., Hayes, S., Hemphill, L., Hernandez, J., Hochell, L., T., Hulyk, S., Hume, J., Imo, K., Jackson, A., Jackson, L., Jacob, L., Jaang, H., Johnson, B., Johnson, R., Kalstus, K., Kelly, S., Keys, T., Khan, Z., King, L., Kovar, C., Kowis, A., Kowis, C., Lara, F., Lee, S., LeGall, F. I., Leon, S., Lewis, L., Li, B., Li, Y., Li, Z., Linnell, M., Liu, W., Liu, Y., S., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorensuhawa, L., Lozado, R., Luk, T., Madu, R., Mahoney, C., Malloy, K., Mansouri, D., Mattinez, E., McClelland, H., McPherson, J., Mercadao, C., Milosavljevic, A., Nazarith, L., Ngo, D., Nguyen, M., Norwig-Eastaugh, E., Nott, A., Nazarith, L., Parker, D., Pasternak, S., Patel, B., Patel, V., Paul, H., Perez, A., Perez, L., Petrosino, J., Pham, T., Patel, P., Pul, L.-L., Pater, J., Reuter, M., Richards, S., Rives, C., Rodriguez, F., Rojas, A., Ruiz, S.J., Sana, M., Sanders, W., Santibanez, J., Santos, R., Sartek, A., Taylor, E., Taylor, T., Thomas, N., Thorn, R., Thornton, R., Trejos, Z., Usmani, K., Varkub, S., Walter, B., Wang, Q., Wang, S., Warten, J., Walter, B., Wang, Q., Wang, S., Warten, J., Walter, S., and G., Willasana, D., Vikk, D., Volkov, A., Walter, B., Mang, Q., Wang, S., Warten, J., Walter, S., and G., Bibbs, R.
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On Aug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-AUG-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-JUL-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 236115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Beltran,B., Beltran,R., Beraducci,A., Biswalo,K., Blyth,P.,
Bonham,H., Buhay,C., Burch,P., Cadoree,I., Canada,A., Cardenas,V.,
Carter,K., Cavazos,I., Chacko,J., Chahrour,M., Chavez,D., Chen,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aug 20, 2004 this sequence version replaced gi:50838862.
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 235518 bases at least Q40 Consensus quality: 235500 bases at least Q30 Consensus quality: 235613 bases at least Q30 Estimated insert size: 251101; sum-of-contigs estimation Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 236115)
                                                                                                                                                                                                                                                                                                 Center project name: PERO Center clone name: CH240-109B14 Center Summary Statistics Sequencing vector: Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weinstock, G. and Gibbs, R.
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TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

Search completed: April 10, 2006, 16:19:54 Job time : 1134.5 secs

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REFERENCE

TITLE JOURNAL

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ORIGIN
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                                                                                                                                  Local Similarity
71982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone

* The sequence data in this record represents an 'enhanced' version

* of a Phase 2 submission. The indicated order and orientation of

* each sequence has been established using one or more of the

* following: read-pair data from individual subclones, overlaps

* with neighboring clones, alignment with available reference

* sequence (e.g., human), and/or confirmation by PCR testing.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence...11 he conticed
                                                                                                      17;
                                               2 TGACCCCGCCCCTGGTC 18
reacccccccccccccrccrc 71998
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1 29106: contig of 29106 bp in length 29107 29606: gap of 500 bp 29607 157023: contig of 127417 bp in length 157024 157043: gap of 20 bp 157044 236115: contig of 79072 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence will be replaced
                                                                                                      Conservative
                                                                                                                                                                                                                                                              /estimated_length=20
157044. 236115
                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig45"
157024. .157043
/note="assembly_name:gap"
157024. .157043
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29607. .157023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-109B14"
                                                                                                                                                                                                                                     note="assembly_name:Contig44"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_name:Contig43"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .236115
                                                                                                   85.0%; Score 17; DB 14;
100.0%; Pred. No. 2.1e+03;
tive 0; Mismatches 0;
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                                                                                                                                                     Length 236115;
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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Perfect score:
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1: /SIDS5/ptodata/2/pubpna/US06 NEW PUB.seq:*

2: /SIDS5/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /SIDS5/ptodata/2/pubpna/US07 NEW PUB.seq:*

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10 US-10-301-480-563398
10 US-10-301-480-1176807
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10 US-10-932-182A-2199
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10 US-10-301-480-571148
10 US-10-301-480-1184557
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Sequence 49068, A
Sequence 999, App
Sequence 997, App
Sequence 1003, Ap
Sequence 1001, App
Sequence 1001, App
Sequence 153398,
Sequence 2199, App
Sequence 2199, Ap
Sequence 2199, Ap
Sequence 11845,
Sequence 11845,
Sequence 11845,
Sequence 21541, App
Sequence 21431, A
Sequence 21541, A
Sequence 21541, A
Sequence 21541, A
Sequence 21541, A
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71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	72.0	72.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0
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Sequence 394, App		Sequence 802285,			12106,		12032,	Sequence 9462, Ap	Sequence 103670,	_	61618,		13222,		Sequence 813651,	æ			Sequence 923657,	Sequence 950510,	Sequence 930079,	Sequence 473525,	Sequence 473524,	Sequence 107498,	Sequence 483357,	Sequence 71202, A

ALIGNMENTS

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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
FRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 49068
FULCTH: 1698
             RESULT 2
US-10-750-623-49068
; Sequence 49068, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-49068
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US-10-750-185-49068
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Best Local S
Matches 18
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENVELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
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APPLICANT: MMI GENOMICS, INC
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18; Conserv
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nilarity 90.0%;
Conservative
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Pred. No. 27;
0; Mismatches
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; ORGANISM: Bovine
US-10-750-623-49068
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TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE MMI100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2003-12-1
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 4968
LENGTH: 1698
                                                           NAME/KEY: CDS
LOCATION: (1)
3-10-453-372-999
                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 999
Query Match
Best Local Similarity
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Best Local
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
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CURRENT FILING DATE: 2003-06-03
                                                                                                                                                             LENGTH: 21
TYPE: DNA
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                                                                                                                     ORGANISM: Homo sapiens FEATURE:
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FILING DATE: 2000-05-31
APPLICATION NUMBER: 09/939398
FILING DATE: 2001-08-24
APPLICATION NUMBER: 60/227800
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KERR, Richard
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HOLM, Tom
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5. US20060003323A1
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90.0%;
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90.0%; Pred. No. 27
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  Score 16.8;
Pred. No. 26;
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RESULT 4
US-10-453-372-997
US-10-453-372-997
Sequence 997, Applica
Publication No. US200
GENERAL INFORMATION:
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APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NU
FILE REFERENCE: 21402-889 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/185967
PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
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SEQ ID NO 997
LENGTH: 2153
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
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CURRENT FILING DATE: 2003-06-03
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PRIOR APPLICATION NUMBER: 60/227800
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PRIOR FILING DATE: 2001-03-19
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                                                                                                                                                                                                                                                                                                                                                                                 1265 GGTCCCGTCAAGGGCACTCT 1284
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Pred. No. 26;
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; NAME/KEY: CDS
; LOCATION: (105)..(5810)
US-10-453-372-1003
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                               Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 1001
LENGTH: 15660
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
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CURRENT FILING DATE: 2003-06-03
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SOFTWARE: CuraSeqList version 0.1
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FILE REFERENCE: 21402-589 A
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TYPE: DNA
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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FILING DATE: 2000-05-31
APPLICATION NUMBER: 09/939398
FILING DATE: 2001-08-24
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APPLICATION NUMBER: 60/195792
FILING DATE: 2000-03-10
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FILING DATE: 2000-05-31
APPLICATION NUMBER: 09/939398
FILING DATE: 2001-08-24
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FILING DATE: 2001-03-19
APPLICATION NUMBER: 60/199476
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APPLICATION NUMBER: 60/195792
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Pred. No. 2

    See File Wrapper or PALM

                                                                                                           See File Wrapper
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Sequence 19, Application US/11065695
Publication No. US20060024688A1
GENERAL INFORMATION:
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FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: 439, 501, 504, 51
LOCATION: 514, 515, 516, 5
LOCATION: 526, 527, 528, 5
LOCATION: 538, 539, 540,
                                                                                                                                            NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 563398
                                                                                                                                                                                                                                                                                                                                                              Sequence 563398, Application US/10301480 Publication No. US20060057564A1
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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TITLE OF INVENTION: ALTERATIONS OF FIBULIN
FILE REFERENCE: IOMA:0580S
CURRENT APPLICATION NUMBER: US/11/065,695
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: 60/547,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2004-02-24 NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (23
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LOCATION:
                                                                                                ORGANISM: Homo
                                                                                                                    TYPE: DNA
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Local Similarity 90.0%;
es 18; Conservation
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Pred. No. 21;
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Pred. No. 22;
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; LOCATION: 596, 597, 598, 599, 600,
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-1176807
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Best Local S
Matches 16
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Matches
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TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FREUERG for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 63
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LOCATION: 596, 597, 598, 599, 600,
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                      LOCATION: 549, 550, 551, 552, LOCATION: 561, 562, 563, 564, LOCATION: 573, 574, 575, 576, LOCATION: 585, 586, 587, 588, OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                  LOCATION: 439, 501, 504, 505, 506, LOCATION: 514, 515, 516, 517, 518, LOCATION: 526, 527, 528, 529, 530, LOCATION: 538, 539, 540, 541, 542, OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapien
                                                                                                                                                             FEATURE:
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                                                                Similarity
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 CCGTCACGCGCACTCT 332
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                                                   80.0%; Score 16;
larity 100.0%; Pred. No.
Conservative 0; Mismatc
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Sequence 2199, Application US/10932182A

| Publication No. US20060046253A1
| GENERAL INFORMATION:
| APPLICANT: NAKAO, YOSHIHIRO
| APPLICANT: NAKAO, YOSHIHIRO
| APPLICANT: NAKAMURA, NORIHISA
| APPLICANT: CODAMA, YUKIKO
| APPLICANT: FUJIMURA, TOMOKO
| APPLICANT: ASHIKARI, TOSHIHIKO
| TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
| FILE REFERENCE: 030685-043
| CURRENT APPLICATION NUMBER: US/10/932,182A
| CURRENT FILING DATE: 2004-09-02
| NUMBER OF SEQ ID NOS: 197023
| SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-932-182A-2199/c
US-10-932-182A-2199/c
; Sequence 2199, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
                                                                                                                                                                                             RESULT 12
US-10-301-480-571148/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA ; ORGANISM: Saccharomyces pastorianus US-10-932-182A-2199
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US-10-932-182A-2199/c
Sequence 571148, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
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SEQ ID NO 2199
LENGTH: 924
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LENGTH: 924
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: NAKAWURA, NORIHISA
APPLICANT: KODANA, YUKIKO
APPLICANT: KUDANA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
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Pred. No. 2e+02;
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Pred. No. 2e
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APPLICANT: Geraci, Mark
APPLICANT: Bull, Todd
APPLICANT: Woelkel, Norbert
APPLICANT: Coldren, Chris
ITILE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene
ITILE OF INVENTION: Expression Analysis of Peripheral Blood Cells
ITILE REFERENCE: 2848-54
CURRENT APPLICATION NUMBER: US/11/122,329
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/568,129
PRIOR APPLICATION NUMBER: 60/568,129
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 128
SOPTWARE: Patentin version 3.3
SEQ ID NO 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 571148
; LENGTH: 974
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; ORGANISM: Homo sapien
US-10-301-480-571148
                                                                                                                                                                                                                                                                                                                                                                               US-11-122-329-125/c
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                   Sequence 125, Application US/11122329 Publication No. US20060019272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1184557
LENGTH: 974
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Best Local S
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Best Local :
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TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapien
-10-301-480-1184557
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TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR PILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
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l Similarity 85.0%;
17; Conservative
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Pred. No. 1.9e+02;
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 974;
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Sequence 1690, Application US/10506454
Publication No. US20060068386A1
GENERAL INFORMATION:
APPLICANT: Slesarev, Alexi I
APPLICANT: Mezhevaya, Katja V
APPLICANT: Polushin, Nikolai N
APPLICANT: Shcharbinina, Olga V
Search completed:
Job time : 313.5 :
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US-10-506-454-1690/c
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                                                                                                                                             Best Local Similarity
Matches 17; Conservat
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APPLICANT: Kozyavkin, Sergei A
APPLICANT: Kozyavkin, Sergei A
TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogens
TITLE OF INVENTION: and Methods of Use Thereof
TITLE REFERENCE: FID001
CURRENT REPLICATION NUMBER: US/10/506,454
CURRENT FILING DATE: 2004-08-31
RIOR APPLICATION NUMBER: PCT/US03/06664
PRIOR PILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: 60/361,742
PRIOR APPLICATION NUMBER: 60/361,742
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 1722
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 1722
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                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Methanopyrus kandleri
                                                                                                                                                                                                                                                                                LENGTH: 1694969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.0%;
Local Similarity 85.0%;
es 17; Conservative
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                                                                        GGTCCCGTCTCGAGCACGCT 303048
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Malykh, Andrei G
: April 10, 2006, 15:25:06 secs
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Pred. No. 1.8e+02;
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Pred. No. 93
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Result
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
   seq length: 0
seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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   GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration
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7
                                 US-10-425-115-87910
US-10-138-588-17
US-09-814-353-21856
US-10-719-993-416
US-10-450-763-3924
US-10-019-065A-34
US-10-115-479-87
US-10-934-998-177
US-10-934-998-177
US-10-114-153-87
US-10-114-153-87
US-10-114-153-85
US-10-934-998-53
US-11-049-637-3
                                                                                                                                                                      US-09-735-995-60

US-10-696-708-60

US-10-944-998-252

US-10-719-993-6589

US-10-719-993-6593

US-10-719-993-41420

US-10-719-993-41474

US-10-934-998-131
             US-10-138-588-19
US-11-049-637-1
                                                                                                                                                                                                                                                                                                                  SUMMARIES
Sequence 60, Appl
Sequence 252, App
Sequence 6589, Ap
Sequence 41474, A
Sequence 41474, A
Sequence 87910, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 3924, Ap
Sequence 87, Appl
Sequence 52, Appl
Sequence 52, Appl
Sequence 52, Appl
Sequence 52, Appl
Sequence 1, Appl
Sequence 27, Appl
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76.0	76.0	76.0	76.0	77.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	80.0	84.0	84.0	84.0	84.0	84.0
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US-10-425-115-115036	US-10-425-115-47123	US-10-029-386-9824	US-10-424-599-135092	US-11-097-143-26002	US-10-156-761-1	US-10-668-767-1	US-10-668-767-143	US-10-668-767-129	US-10-668-767-127	US-10-668-767-145	US-11-097-143-18580	US-11-097-143-18581	US-10-282-122A-32124	US-10-437-963-89641	US-10-425-115-158984	US-10-311-455-1235	US-10-719-993-6892	US-10-723-860-5390	US-10-773-446-66	US-10-934-998-30	US-10-980-387-27
Sequence 115036,	Sequence 47123, A	Sequence 9824, Ap	Sequence 135092,	Sequence 26002, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 143, App	Sequence 129, App	Sequence 127, App	Sequence 145, App	Sequence 18580, A	Sequence 18581, A	Sequence 32124, A	Sequence 89641, A	Sequence 158984,	Sequence 1235, Ap	Sequence 6892, Ap	Sequence 5390, Ap	Sequence 66, Appl	Sequence 30, Appl	Sequence 27, Appl

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/735,995
COURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/226,012
PRIOR FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-735-995-60
US-10-96-708-60
US-10-96-708-60
Sequence 60, Application US/10696708
Publication No. US20040078833A1
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
ITITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG TITLE OF INVENTION: SYNDROME GENE
FILE REFERENCE: 2323-164
CURRENT APPLICATION NUMBER: US/10/696,708
CURRENT APPLICATION NUMBER: US/10/696,708
PRIOR APPLICATION NUMBER: US/9/735,995
PRIOR APPLICATION NUMBER: US/9/735,995
PRIOR APPLICATION NUMBER: US/9/726,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60, Application US/0973;
Patent No. US20010034024A1
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: MUTATIONS II
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Best Local
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APPLICANT: AL-MAHNOOD, SALMAN
APPLICANT: COLIN, SYLVIE
APPLICANT: COLIN, SYLVIE
APPLICANT: COLIN, SYLVIE
APPLICANT: COLIN, SYLVIE
TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIGGENESIS, PHARMACEUTICAL
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
FILE REFERENCE: BMA-04-1206
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT APPLICATION NUMBER: PCT/FR03/0695
PRIOR APPLICATION NUMBER: PCT/FR03/0695
PRIOR FILING DATE: 2003-03-04
PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: FR02/02717
PRIOR APPLICATION NUMBER: FR02/04716
PRIOR APPLICATION NUMBER: FR02/04546
PRIOR APPLICATION NUMBER: FR02/04546
PRIOR APPLICATION NUMBER: S002-04-01
SOFTWARE: PASCANDAME
PRIOR APPLICATION NUMBER: S002-04-11
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PASCANDAME
PRIOR FILING DATE: 2002-04-12
SEQ ID NO 252
LENGTH: 29
TYDER: DAM
Sequence 6589, Application US/10719993

Publication No. US20040265849A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS:
TITLE OF INVENTION: ALTHEIMER'S DISEASE, ME:
FILE REFERENCE: CL001496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6589

LENGTH: 201
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US-10-719-993-6589
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US-10-934-998-252
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-696-708-60
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Matches
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PRIOR APPLICATION NUMBER: 09/122,847
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 252, Application US/10934998 Publication No. US20050153917A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: PCR primer GV29-1
-10-934-998-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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nilarity 90.0%;
Conservative
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                                                                                                                                                                           ASSOCIATED METHODS OF
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DETECTION AND USES
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Sequence 41420, Application US/1071993

Publication No. US20040265849A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERIC CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOMBER: S5342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41420
LENGTH: 201
TYDE: DNA
ORGANISM: Homo sapiens
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US-10-719-993-6593
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Publication No. US20040265849A1

Publication No. US20040265849A1

Publication No. US20040265849A1

APPLICANT: CARGILL, Michele et al.

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 6593

LENGTH: 2011
                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
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Best Local Similarity
                                                                  Matches
181 GGTCCTGTCAGGCGCACTCT
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                    1 GGTCCCGTCACGCGCACTCT
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                                                                  Conservative
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90.0%;
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Pred. No. 8
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Pred. No. 8
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Pred. No. 87;
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RESULT 7 US-10-719-993-41474 ; Sequence 41474, Application US/10719993 ; Publication No. US20040265849A1

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US-10-425-115-87910
; Sequence 87910, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-934-998-131
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-41474
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: ACCHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLUO1496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41474
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Best Local
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                APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallc, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SCHNEIDER, CHRISTOPHE
TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
FILE REFERENCE: BWA-04-1206
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: PCT/FR03/00695
PRIOR FILING DATE: 2003-03-04
PRIOR PHILING DATE: 2003-03-04
PRIOR PHILING DATE: 2003-03-04
PRIOR PHILING DATE: 2002-04-11
PRIOR PHILING DATE: 2002-04-11
PRIOR FILING DATE: 2002-04-11
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SOFTWARE: PatentIn version 3.2
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CURRENT APPLICATION NUMBER: US/10/425,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 564
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Similarity 90.0%;
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; Pred. No. 87;
0; Mismatches
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Pred. No. 77;
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; ORGANISM: Homo (); FEATURE: ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (16)... US-10-138-588-17
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Best Local Similarity
Watches 18; Conserve
                                                                                                                                                                                                                                                                                                         RESULT 11
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                                                                                                                                                                                                                                                                                    US-09-814-353-21856
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LENGTH: 1851
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
JENERAL INFORMANCE TOWN APPLICANT: Lee, John APPLICANT: Lee, John APPLICANT: Thompson, Pamela APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/99/814,353
                                                                                                                                                                                                                       Sequence 21856, Application US/09814353 Publication No. US20030165831A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 18; Conserv
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SEQ ID NO 17
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CURRENT APPLICATION NUMBER: US/10/138,588

CURRENT FILING DATE: 2002-05-01

PRIOR APPLICATION NUMBER: 60/288,395

PRIOR FILING DATE: 2001-05-03

PRIOR APPLICATION NUMBER: 60/308,901

PRIOR APPLICATION NUMBER: 60/313,388

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 2001-08-17
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NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/288,900 PRIOR FILING DATE: 2001-05-04
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PRIOR FILING DATE: 2001-09-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Pred. No. 66;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8;
Pred. No. 6
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RESULT 13
US-10-450-763-3924
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-416
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 416, Application US/10719993

Publication No. US20040265849A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETEC

FILE REFERENCE: CL001496
                                                                                                                                      Sequence 3924, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                     Matches
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APPLICANT: HYSSEG, INC
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2, 3, 4, 5, 247, 3407
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/191,031
FILING DATE: 2000-03-21
APPLICATION NUMBER: US 60/207,124
FILING DATE: 2000-05-25
APPLICATION NUMBER: US 60/211,940
FILING DATE: 2000-06-15
FILING DATE: 2000-06-15
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18; Conservative
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Similarity 90.0%;
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Pred. No. 61;
0; Mismatches
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-019-065A-34
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US-10-115-479-87
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PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSCOM
SEQ ID NO 3924
LENGTH: 3910
TYPE: DNA
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Publication No. US20040086501A1
                                                                                                                                             APPLICANT: Li, Li
APPLICANT: Gerlac
APPLICANT: Liu, X
APPLICANT: Miller
                                                                                                                                                                                                                           Sequence 87, Application US/10115479 Publication No. US20040006205A1
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Best Local Similarity
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TITLE OF INVENTION: Protein Having Activity
FILE REFERENCE MSB-7265-PCT
CURRENT APPLICATION NUMBER: US/10/019,065A
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/266,300
PRIOR APPLICATION NUMBER: US 60/266,300
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 34
                                                                APPLICANT:
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NAME/KEY: SIMILAR
LOCATION: (3497)...(3649)
OTHER INFORMATION: 29% homologous to Caenorhab
OTHER INFORMATION: precursor,accession number
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                                                                                            Liu, Xiaohong
Miller, Charles E.
Spytek, Kimberly A.
Zerhusen, Bryan D.
Pena, Carol E.A.
Shenoy, Suresh G. Zhong, Haihong Smithson, Glendda Casman, Stacie J. Boldog, Ferenc L.; Voss, Edward
                                                                                                                                                                              Gerlach, Valerie L.
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90.0%;
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Pred. No. 6
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Pred. No. 60;
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APPLICANT:

APPLICANT:

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APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Meses, Peter S.
APPLICANT: Hursh, Katarzyna
APPLICANT: Burgess, Catherine E.
APPLICANT: Meses, Peter S.
APPLICANT: Mayanker, Uriel M.
APPLICANT: Mayanker, Uriel M.
APPLICANT: Mayanker, Uriel M.
APPLICANT: Mayanker, Shlomit R.
APPLICANTON UNMERE: US/10/115,479
CURRENT APPLICATION UNMERE: US/281,165
PRIOR APPLICATION UNMERE: GO/281,863
PRIOR APPLICATION UNMERE: GO/283,657
PRIOR APPLICATION UNMERE: GO/283,657
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PRIOR APPLICATION UNMERE: GO/283,679
PRIOR APPLICATION UNMERE: GO/283,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 87
LENGTH: 5935
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (1)..(5860)
US-10-115-479-87
Search completed: April 10, 2006, 15:20:58 Job time : 448 secs
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCOMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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467.779 Million cell updates/sec
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Listing first 45 summaries
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ALIGNMENTS

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APPLICANT: Keating, Mark T.

APPLICANT: Splawski, Igor
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A
TITLE OF INVENTION: SYNDROME GENE
FILE REFERENCE: 2323-136
CURRENT APPLICATION NUMBER: US/09/226,012
CURRENT FILING DATE: 1999-01-06
EARLIER APPLICATION NUMBER: 09/122,847
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 20
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US-09-953-096-3
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-226-012-60
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US-09-226-012-60
Sequence 3, Application US/0953096
Patent No. 6867291
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Mathur, Brian
APPLICANT: Donoho, Gregory
TITLE OF INVENTION: No. 6867291e1 Human Hemicentin Proteins and Polynucleotides Encod
FILE REFERENCE: LEX-0235-USA
CURRENT APPLICATION NUMBER: US/09/953,096
CURRENT APPLICATION NUMBER: US/09/953,096
CURRENT APPLICATION NUMBER: US 60/232,793
PRIOR APPLICATION NUMBER: US 60/232,793
PRIOR FILING DATE: 2000 09-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 20; Conserv
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GENERAL INFORMATION:

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Mathur, Brian

APPLICANT: Donoho, Gregory

ITILE OF INVENTION: NO. 6867291el Human Hemicentin Proteins and

FILE REFERENCE: LEX-0235-USA

CURRENT APPLICATION NUMBER: US/09/953,096

CURRENT FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: US 60/232,793

PRIOR FILING DATE: 2000 09-15

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                        ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10499
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; Sequence 10499, Application US/09270767
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Matches 18
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Matches
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10499
LENGTH: 652
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TYPE: DNA
ORGANISM: homo sapiens
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Local Similarity 90.0%;
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Pred. No. 54
                                                         Score 15.8; DB 3;
Pred. No. 1.7e+02;
0; Mismatches 2;
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20356
LENGTH: 1196
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 4679

LENGTH: 711

TYPE: DNA
ORGANISM: Klebsiella pneumoniae
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; ORGANISM: Drosophila melanogaster
US-09-270-767-5074
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US-09-270-767-5074/c
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Sequence 4679, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5074
                                                                                                                                                                                                                                     Sequence 20356, Appl:
Patent No. 6703491
GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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Matches 17; Conserv
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ORGANISM: Drosophila melanogaster -09-270-767-20356
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89.5%;
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Pred. No. 1.7e+02;
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                                                                                                                                                                                                  of Drosophila melanogaster
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RESULT 8
US-09-621-976-3072/c
                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: Patent.pm
SEQ ID NO 3072
                                                                                                                                                                                    SOFTWARE: FastS
SEQ ID NO 142055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 142055, A Patent No. 6812339
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Best Local
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Best Local
                                                     Matches
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TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 452
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                    LENGTH: 601
TYPE: DNA
ORGANISM: Human
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LOCATION: 16..240
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17; Conserv
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1 GGTCCCGTCACGCGCACTCT 20
                                                   l Similarity
17; Conserv
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                                                   76.0%; llarity 85.0%; Conservative
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Pred. No. 2.6e+02;
0; Mismatches 1
                                                                  Score 15.2; DB 3;
Pred. No. 3.2e+02;
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Pred. No. 3.2e+02;
0; Mismatches 3;
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                                                                                  Length 601;
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; Sequence 70, Application US/09775398
; Patent No. 6893820
; GENERAL INFORMATION:
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US-08-240-372-1/c
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LENGTH: 994
TYPE: DNA
ORGANISM: Homo sapiens 4.D.12
                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08240372
Patent No. 5741665
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         COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (754)...(754)
OTHER INFORMATION: a or
NAME/KEY: n
LOCATION: (764)...(764)
OTHER INFORMATION: a or
                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: KATO, ELLE K.
APPLICANT: STUART, W. DORSEY
APPLICANT: STUART, W. DORSEY
TITLE OF INVENTION: LIGHT-REGULATED PROMOTERS FOR PRODUCTION
TITLE OF INVENTION: OF HETEROLOGOUS PROTEINS IN FILAMENTOUS FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/775,398
CURRENT FILLING DATE: 2001-01-04
NUMBER OF SEQ ID NOS: 90
SOPTWARE: Patentin version 3.0
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TITLE OF INVENTION: Detection of Methylated CpG Rich Sequences Diagnostic for Maligna
FILE REFERENCE: 22727/04075
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NAME/KEY: n
LOCATION: (673)..(673)
OTHER INFORMATION: a or
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LOCATION: (774)..
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LOCATION: (
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                                                                                                                         STREET: 2000
CITY: Washington, I
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                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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FILING DATE:
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Pred. No. 3.2e+02;
0; Mismatches 3
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                                           Version
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; Sequence 1090, Application US/09902540; Patent No. 6833447
                                      RESULT 13
US-09-902-540-1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-668-680-12
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                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (1)..(1338)
3-09-668-680-12
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Best Local 9
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Best Local S
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aldong J.
APPLICANT: Xu, Chongjun
APPLICANT: Drmanac, Radoje T.
APPLICANT: No. 6436703el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIPZA
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 13
SOFTWARE: pt_FL_genes Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/668,680
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
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INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 1237 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
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                                                                                                                     720 GGTCCCGCCACGGGCCCTCT 739
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Similarity 85.0%;
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Similarity 85.0%;
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Liu, Chenghua
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Pred. No. 3.2e+02;
0; Mismatches 3;
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US-09-949-016-12415/c

; Sequence 12415, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR APPLICATION NUMBER: 60/237,768
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; ORGANISM: Myxococcus xanthus
US-09-902-540-9597
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US-09-902-540-9597
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NO 1090
LENGTH: 14462
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Matches 17; Conservative
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Matches 17; Conserv
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LENGTH: 14462
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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nilarity 85.0%;
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Pred. No. 3.2e+02;
0; Mismatches 3;
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OF DETECTION AND USES
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 Listing first 45 summaries
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  9177750
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0 CZ917270
0 CG464694
                           BB207204
BB207204
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BG208296
CK685362
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598.492 Million cell updates/sec
CZ917270 4021005A0
CC9464694 KRIBB 2D
BE207204 bal3e01.y
BF059067 7k37d02.x
AQ338091 HS 5011 B
CK679806 ZF101-P00
CK679806 ZF101-P00
DR448434 AR1055F05
DR442497 AR2005D08
CN200871 TOV10541
CN200871 TOV10541
CN200873 TOV1059 G
CG003293 ZUAEY27TV
CN206743 TOV7169
CG390264 ZMMBB0057
BU747235 TOV73313 G
CG390264 ZMMBB0057
BU747235 TOV5324 G
CC39026786 ACENCOURT
CN209177 TOV9445 G
CC300703 ZMMBF00074
CC649591 OGWCH17TV
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BU283768	BM684541	AQ658336	CG186409	AQ941653	TA356A01P	TA317D09Q	AJ234088	BG075801	B54696	W15079	TA134F11Q	CW925592	CNS 04GO3	CC643968	CC643962	BI955119	BF670386	DQ037949	DQ037948	HSM804543	CL285801	CZ334451
BU283768 603864203	BM684541 UI-E-EJO-	AQ658336 Sheared D	CG186409 PUIGL56TD	AQ941653 Sheared D	AL497090 T. brucei	AL491463 T. brucei	AJ234088 B927 036	BG075801 H3152A03-	B54696 CIT-HSP-384	W15079 T1726 MVAT4	AL466343 T. brucei	CW925592 EDCBB53TF	AL289884 Tetraodon	CC643968 OGQAC36TM	CC643962 OGQAC36TC	BI955119 HVSMEm002	BF670386 602150266	DQ037949 Pan trogl	DQ037948 Homo sapi	AL833232 Homo sapi	CL285801 ZMMBBb063	CZ334451 ZMMBF0043

ALIGNMENTS

RESULT 1 H21884 LOCUS DEFINITION ACCESSION VERSION KEYWORDS REFERENCE AUTHORS SOURCE ORGANISM COMMENT FEATURES source The Washi-Merck EST Project Unpublished (1995)
Contact: Wilson RK
Washington University School (4444 Forest Park Parkwey, Box Tel: 314 286 1800
Fax: 314 286 1810 Email: est@watson.wustl.edu
Insert Size: 951
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLML
This clone is available royalty-free through LLML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 951 Std Exror: 0.00
Seq primer: M13RP1 1 (bases 1 to 211)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and H21884 211 bp mRNA linear EST 06-JUL yl34e11.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:160172 5' similar to SP:NCA3 MOUSE P13594 NEUVAL CELL ADHESION PROTEIN, SECRETED ISOFORM PRECURSOR ;, mRNA sequence. H21884.1 Wilson, R. Hominidae; Homo. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens Homo sapiens (human) quality sequence stop: 1.
Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:578597" /db_xref="taxon:9606" GI:890579 Sol of Medicine Box 8501, St. Louis, MO 63108 Marra, M., EST 06-JUL-1995

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REFERENCE
AUTHORS
TITLE
JOURNAL
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SOURCE
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCCCGTCAAGGGCACTCT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 walbot@stanford.edu
4021005 column: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transposon-tagged
                                                                                                                  // / dev stage="adult"
//dev stage="adult"
//dev stage="adult"
//lab_host="pH10B"
//clone lib="4021 - RescueMu Grid V"
//clone lib="4021 - RescueMu Grid V"
//clone lib="4021 - RescueMu (engineered from pR10 photo="Organ: leaf; Vector: RescueMu (stage li);
//clone lib="4021 - RescueMu (engineered from pR11;
//clone lib="4021 - RescueMu (engineered from prince li);
//clone lib="4021 - RescueMu (engineered from pR11;
//clone lib="4021 - RescueMu (engineered from prince lib="4021 - R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                v was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library constructed by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:160172"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.0%;
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Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
and then
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screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 211;
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FEATURES

Query Match Best Local Similarity

84.0%;

Score 16.8; DB 10; Pred. No. 1.4e+03;

Length 387;

COMMENT

RESULT 2 CZ917270 LOCUS

VERSION

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ORIGIN

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JOURNAL COMMENT
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VERSION
KEYWORDS
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LOCUS
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 bp DNA linear GSS :
KRIBB 2D B25T7 pBS-NE Library Homo sapiens genomic clone
KRIBB 2D B25 5, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@kribb.re.kr
This result was produced by the program for Functional Analysis of
Human Genome funded from Ministry of Science and Technology,
Republic of Korea. Clones are available from the Center for
Functional Analysis of Human Genome. See URL:
http://2logenome.kribb.re.kr/ for details or contact:
yongsung@kribb.re.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Genome Research Laboratory
Korea Research Institute of Bioscience and Biotechnology
52 Eoeun-dong, Yuseong-gu, Daejeon 305-333, Republic of Korea
Tel: 82-42-879-8110
Fax: 82-42-879-8119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 387)
Lee, K.T., Kim, J.H., Hahn, Y.S., Yang, J.O., Chu, M.Y., Oh, K.J., Xim, S., Yoo, H.S. and Kim, Y.S.
Rapid isolation of NotI-linked CpG island sequences Unpublished (2003)
Contact: KIM YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGTCCCGTCACGCGCACTCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 387.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG464694.1 GI:35188129
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCCGGTCACGCGCACTCT 214
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                                                              /dev_stage="adult"
/clone lib="pBS-WE Library"
/clone lib-
/clone lib="pBS-WE Library"
/clone lib-
/clone 
                                  transformed into DH5a cell using electroporation machine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ampicillin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.0%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Pred. No. 1.5e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS 24-SEP-2003
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BE207204/c
                                                                                            RESULT 5
BF059067/c
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                     ACCESSION
                                                           DEFINITION
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                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library

Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 493)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE207204 493 bp mRNA linear EST 27-JUN-2000 bal3e01.y1 NIH MGC 7 Homo sapiens CDNA clone IMAGE:2824248 5' similar to WP:T08B2.9 CE13435 PHENYLALANYL-TRNA SYNTHETASE ;, mRNA
mRNA sequence.
BF059067
BF059067.1 GI:10812963
                                             BF059067
7k37d02.x1 NCI_CGAP_Ov18 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality Seq primer: -40RP from Gibco High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE207204.1 GI:8750602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                            GGTCCCGTCACGCGCACTCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCCTGTCAGGCGCACTCT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCCCGTCACGCGCACTCT 20
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE:2824248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 493
                                                                                                                                                                                                                                                                 84.0%;
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                                                                                                                                                                                                                                                <u>.</u>
                                                                                                                                                                                                                                                                 Score 16.8; DB 2; Length 493; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                    Mismatches
                                                       507 bp mRNA linear EST 16-OCT-
Homo sapiens cDNA clone IMAGE:3477554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲.
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                                                                          EST 16-OCT-2000
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AQ338091
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Matches
                     JOURNAL
                                                           TITLE
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                   Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                      Hominidae; Homo.

1 (bases 1 to 534)

Mahairas,G.G., Wallace,J.C.,
Keller,A., Shaker,R., Furlong
                                                                                                                                                                                                                                                                                     AQ338091 534 bp DNA linear GSS 06-MA
HS 5011 B1 A04 T7 RPCI11 Human Male BAC Library Homo sapiens
genomic clone Plate=587 Col=7 Row=B, genomic survey sequence.
AQ338091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGTCCCGTCACGCGCACTCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Micha
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                            Homo sapiens
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: '
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.

1 (bases 1 to 507)
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                                                                                                                                                                                                                                                                   AQ338091.2 GI:4341992
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3477554"
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                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleo Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.8;
Pred. No. 1.
                                                                                            Furlong, J., Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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1.4e+03;
                                                                                              Young
                                                                                            Swartzell,S.,
g,J., Zhao,S.,
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                                                                                                Holzman, T.,
Adams, M.D. and
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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGTCCCGTCACGCGCACTCT 20
                                                                                                                           Plate: ZF101-P00037-BR2 row: D
Seq primer: CCGCATAACTTGTATAGCA
High quality sequence stop: 547.
                                                                                                                                                                                                                                                                     Cloning and Sequencing
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome,
Tel: +65 6478 8073
Fax: +65 6478 9059
                                                                                                                                                                                                                                                                                                                                                                              Wei,C., Mathavan,S., Thoreau,H., Lim,L., Genome Institute of Singapore, Zebrafish Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CK685362

ZF101-P00037-DEPE-F2_D17 GISZF001_ra Danio rerio cDNA clone
IMAGE:7147939 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 587 row: B column: 7
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Feb 19, 1999 this sequence version replaced gi:4144107. Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                   Email: ruanyj@gis.a-star.edu.sg
GIS Clone ID: ZF101-P00037-BR2_D17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                   BACKWARD: M13
                                                                                                                                                                                                    FORWARD: M13
                                                                                                                                                                                                                 PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                  Contact: Ruan
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 547)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CK685362.1 GI:42437698
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db xref="taxon:5906"
/clone="Plate=587 Col=7 Row=B"
                  /organism="Danio rerio"

(mol_type="mRNA"

(strain="Singapore local strain"

(db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphocytes"
/clone_lib="RPCI11 Human Male BAC Library"
/note="Vector: pBACe3.6; RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="Male"
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                                                                                                            on/Qualifiers
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Pred. No. 1.4e+03;
0; Mismatches 2;
                                                                                                                                                                column: 17
                                                                                                                                                                                                                                                                                                          Singapore 138672
                                                                                                                                                                                                                                                                                                                                                                                                  Lee, C. and Ruan, Y. Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 534;
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AUTHORS
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ORGANISM
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CK679806/c
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KEYWORDS
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                                                           1. .596
/mol_type="mRNA"
/strain="Singapore local strain"
                                     organism="Danio rerio"
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cloned, 5' cloning site: Sfi A site GGCCATTMAGGCC;
linker/adaptor sequence: 5.AAGCAGTGGTATCAACGCCAGAGTGGCC;
3' cloning site: Sfi B site GGCCAAGAGGCCC;
linker/adaptor sequence: same as the priming sequence;
linker/adaptor sequence: same as the priming sequence;
Average insert size: 2kb; For PCR insert analysis: Use
M13 Forward and reverse primers; Library complexity: 5x106;
Recombinants (inserts): 98%; Library complexity: 5x106;
Full-length construction (method): SMART, a Clontech
method The pooled tissue RNA was collected and used to
construct full length enriched CDNA library and also
served as template to synthesize complex first strand cDNA
probe. Two high density colony arrays were made from over
l10K cDNA clones and hybridized with the probes. Low
intensity clones were selected as they represented rare
expressed clones. The hybridization intensities for all
clones span from 0 to 1.8 million counts and the low
abundant class ranged from 0 to 13,000."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="GISZF001 ra"
/clone_Tib="GISZF001 ra"
/note="Vector: pDNR-LIB; Site_1: Sfi A (GGCCATTACGGCC);
Site_2: Sfi B (GGCCGAGGCGGCC); Priming method: Sfi-(dT)30
Primed ; Priming sequence:
5.ATTCTAGAGGCCGAGGGCGGCCACATG(T)30VN; Directionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Embryo"
/dev stage="7 Different embryonic Stages(From just
fertilized Embryos to 72 hours just hatched baby fish)"
/lab_host="DH10B"
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307 GGTCCAGTCACGCGCATTCT 288 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 596)
Wei,C., Mathavan,S., Thoreau,H., Lim,L., Lee,C. and Ruan,Y. Genome Institute of Singapore, Zebrafish Gene Collection Unpublished (2004) Cloning and Sequencing
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome, Singapore 138672
Tel: +65 6478 8073
Fax: +65 6478 9059 CK679806 596 bp mRNA linear E ZF101-P00018-DEPE-F NO4 GISZF001_ra Danio rerio cDNA IMAGE:7141254 5', mRNA sequence. Plate: ZF101-P00018-BR2 row: N Seq primer: CCGCATAACTTGTATAGCA Email: ruanyj@gis.a-star.edu.sg GIS Clone ID: ZF101-P00018-BR2_N04 Contact: Ruan Danio rerio (zebrafish) BACKWARD: M13 GGTCCCGTCACGCGCACTCT quality sequence stop: 596 Location/Qualifiers Conservative GI:42431958 84.0%; Score 16.8; DB 7; Pred. No. 1.4e+03; 20 Mismatches column: 04 DB 7; Length 547; EST 30-MAR-2004 0, Gaps 0

/tissue_type="Embryo"
/dev stage="7 Different embryonic Stages(From just
fertIlized Embryos to 72 hours just hatched baby fish)"
/lab_host="DH10B"

/db_xref="taxon:7955" /clone="IMAGE:7141254"

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REFERENCE
AUTHORS
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VERSION
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LOCUS
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                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acanthoscurria gomesiana
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Acanthoscurria.
1 (bases 1 to 624)
1 (bases 1 to 624)
1 (bases 1 to 624)
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                                                                                                                                                                                                                                                                                                                                                                       and Daffre,S.
Discovery of immune related genes expressed on hemocytes of the tarantula spider Acanthoscurria gomesiana
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DR448434 624 bp mRNA linear EST 05-JUL-200 AR1055F05 A. gomesiana hemocytes normalized library Acanthoscurria gomesiana cDNA clone AR1055F05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                      Contact: Daffre S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acanthoscurria gomesiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR448434.1 GI:68770098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linker-Adaptor sequence: same as the priming sequence; Average insert size: 2kb; For PCR insert analysis: Use M13 Forward and reverse primers; Library Amplified; Recombinants (inserts): 98%; Library complexity: 5x106; Full-length construction (method): SMART, a Clontech method The pooled tissue RNA was collected and used to construct full length enriched CDNA library and also served as template to synthesize complex first strand cDNA probe. Two high density colony arrays were made from over intensity clones and hybridized with the probes. Low intensity clones were selected as they represented rare expressed clones. The hybridization intensities for all clones span from 0 to 1.8 million counts and the low abundant class ranged from 0 to 13,000."
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5.ATTCTAGAGGCCGAGAGGCGGACATG(T)30VN; Directionally cloned, 5' cloning site: Sfi A site GGCCATTACGGCC; 5' linker/adaptor sequence: 5.AAGCAGTGGTATCAACGCAGAGTGGCC; 3' cloning site: Sfi B site GGCCGAGGCGCC; 3'
                        /organism="Acanthoscurria gomesiana"
/mol_type="mRNA"
/db xref="taxon:115339"
/clone="AR1055F05"
                                                                                                                       1. .624
/tissue_type="hemocytes"
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Site_2: Sfi B (GGCCGAGGCGGCC); Priming method: Sfi-(dT)30
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Pred. No. 1.4e+03;
0; Mismatches 2;
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Best Local S
Matches 18
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                                                                   18;
   1 GGTCCCGTCACGCGCACTCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fal: 55 11 3091 7272
Fax: 55 11 3091 7417
Email: sidafffre@icb.usp.br
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acanthoscurria gomesiana
Acanthoscurria gomesiana
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Mygalomorphae, Theraphosidae, Acanthoscurria.
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AR2005D08 A. gomesiana hemocytes library Acanthoscurria
cDNA clone AR2005D08 5', mRNA sequence
DR442497
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University of Sao Paulo
Av. Prof. Lineu Prestes, 1374, CEP 05508-900, Sao Paulo, SP, Brazil
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DR442497.1 GI:68758988
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Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Discovery of immune related genes expressed on hemocytes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Daffre,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 659)
Lorenzini, D.M., Sil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Daffre S
                                                                                                    Similarity
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Location/Qualifiers
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/dev_stage="adult"
/dev_stage="adult"
/clone_lib="A. gomesiana hemocytes normalized library"
/clone_lib="A. gomesiana hemocytes normalized library"
/note="Vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
normalized cDNA library. first strand synthesis with
NotI-dT(18) primer. cDNAs > 350 bp selected by
chromatography (Bio-Gel A50). double-stranded cDNAs
ligated to EcoRI blunt adapter, digested with NotI, size
selected (> 350 bp) and cloned into pT7T3-Pac vector.
single-stranded plasmids hybridized with cDNA inserts at
low Cot (aprox 5), remaining single-stranded plasmids |
low Cot (aprox 5), remaining single-stranded
                                                                                                                                                                                                                             /clone_lib="A. gomesiana hemocytes library"
/note="Vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
-Pac vector."
                                                                                                                                                                                                                                                                                                                    tissue_type="hemocytes"
/cell_type="hemocytes"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Acanthoscurria
/mol_type="mRNA"
/db_xref="taxon:115339"
/clone="AR2005D08"
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Pred. No. 1.4e+03;
                                                                                                 Score 16.8;
Pred. No. 1.
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                                                                                                 1.4e+03;
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                                                                                                                               Length 659;
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VERSION
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VERSION
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CN208425
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AUTHORS
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CN208425
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.
                                    3810
                                                                                                               1 (bases 1 to 733)
Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauget, S.A. and Payton, P.R.
The rehydration transcriptome of the desiccation-tolerant bryoph
Tortula nuralis: transcript classification and analysis
BMC Genomics 5 (1), 89 (2004)
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Tor8923 Gametophyte rehydrati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 694)
Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
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Tor10541 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.
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                                                                    Plant Stress Lab
                                                                                    Contact: Oliver Melvin J
                                                                                                     15546486
                                                                                                                                                                                                                                                                                     CN208425.1
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806-749-5560
806-723-5272
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4th St, Lubbock,
806-749-5560
806-723-5272
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llarity 90.0%;
Conservative
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/db_xref="taxon:38588"
/clone_lib="Gametophyte rehydration Library"
/note="Organ: Green Gametophyte; Vector: pSp
Sall; Site_2; NotI"
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Pred. No. 1.4e+03;
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RESULT 14 CN206743

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAI

(bases to 737)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R. W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: ZUAEY27TH

Contact: Cathy Whitelaw
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CG003293
CG003293.1
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FORWARD: GTTTTCCCAGTCACGAC
BACKWARD: CAGGAAACAGCTATGAC
Location/Qualifiers
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Fax: 301-838-0208
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                                                                      Similarity
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Sall; Site_2: NotI"
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Pred. No. 1.4e+03
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.

1 (bases 1 to 794)
Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauget, S.A. and Payton, P.R.
The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis; transcript classification and analysis
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FORWARD: GTTTTCCCAGTCACGAC
BACKWARD: CAGGAAACAGCTATGAC.
                                                                      3810 4th St, Lubbock, TX 79415, USA Tel: 806-749-5560
Fax: 806-723-5272
                                                                                                                                                                                                                                                                                                                                                                                                sequence.
CN202185
CN202185.1 GI:46898916
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1 (bases 1 to 793)

Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.

The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
BMC Genomics 5 (1), 89 (2004)
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Tor2313 Gametophyte rehydration
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FORWARD: GTTTTCCCAGTCACGAC BACKWARD: CAGGAAACAGCTATGAC.
                                     PCR PRimers
                                                      Email: moliver@lbk.ars.usda.gov
                                                                                                                                                   Plant Stress Lab
                                                                                                                                                                    Contact: Oliver Melvin J
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Adk60602 Angiogene	ADK60602	12	6024	84.0	16.8	19
Adk60301 Angiogene	ADK60301	12	6024	84.0	16.8	18
Ade16057 G-coupled	ADE16057	10	5935	84.0	16.8	17
Ad193996 Human G-c	ADL93996	12	5877	84.0	16.8	16
Aai72024 Human thr	AAI72024	σ	4073	84.0	16.8	15
Aas68120 DNA encod	AAS68120	Ç	3910	84.0	16.8	14
Adl63644 Human ova	ADL63644	ഗ	3407	84.0	16.8	13
Adc30192 Human nov	ADC30192	10	2517	84.0	16.8	12
Ado08270 Human NOV	ADO08270	12	2153	84.0	16.8	11
Adh72101 Human ger	ADH72101	12	2153	84.0	16.8	10
Aca10119 Human NOV	ACA10119	æ	2153	84.0	16.8	9
Adh72103 Human gen	ADH72103	12	2136	84.0	16.8	œ
Adp73179 Angiogene	ADP73179	12	564	84.0	16.8	7
Adk60556 Antisense	ADK60556	12	564	84.0	16.8	6
Adk60255 Antisense	ADK60255	12	564	84.0	16.8	v
Adp73300 Primer of	ADP73300	12	29	84.0	16.8	4
Adk60677 Angiogene	ADK60677	12	29	84.0	16.8	w
Adk60376 Angiogene	ADK60376	12	29	84.0	16.8	N
Aaa07658 Forward p	AAA07658	w	20	100.0	20	μ
Description	ID	DB.	Match Length	Match	Score	No.
) .		200111

The invention relates to a HERG protein having a mutation compared to wild-type HERG, and is useful for developing products for the diagnosis, prevention and treatment of long QT (LQT) syndrome. The products and methods can be used for the diagnosis of subjects with LQT syndrome. They can also be used to screen for drugs for treating or preventing LQT syndrome. The HERG nucleic acids can also be used for gene therapy and HERG peptides can be used for gene therapy and

Claim 7; Page 72; 163pp; English.

New isolated mutant HERG nucleic acids, useful for developing products for the diagnosis, prevention and treatment of long QT syndrome.

WPI; 2000-195319/17.

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79.0	80.0	80.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0
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Ach98884 Klebsiell			Adl13809 Osteoarth	Adq22570 Human sof	Aeb94344 Human hem	Adp73078 Angiogene	Adk60756 Angiogene	Adk60455 Angiogene	Abq86156 Novel hum	Aeb34665 Human hem	Ady74311 Human hem	Adh72105 Human gen	Aca10120 Human NOV	Ado08272 Human NOV	Aeb34667 Human hem	Ady74313 Human hem	Ads98520 Protein f		Adp73100 Angiogene	Adk60778 Angiogene	Adk60477 Angiogene	Abx56303 Human NOV	Adh72107 Human gen	Abx56304 Human NOV	Adp73225 Angiogene

ALIGNMENTS

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RESULT 1
AAA07658
ID AAA0
Keating MT,
                                                                                                                            27-JUL-1998;
06-JAN-1999;
                                                                                                                                                20-JUL-1999;
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                                                                                                                                                                                                      HERG; mutation; PCR primer; ss.
                                                                                                                                                                                                                        Forward primer for amplifying HERG gene exon 2.
                                                                                                                                                                                                                                      19-JUN-2000
                                                                                                                                                                                                                                                    AAA07658;
                                                                                                                                                                                                                                                                 AAA07658 standard; DNA; 20 BP.
                                                                                                                                                              10-FEB-2000.
                                                                                                                                                                                        Homo sapiens.
                                                                                                               (UTAH ) UNIV UTAH RES FOUND.
                                                                                                  Splawski I;
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                                                                                                                            98US-00122847.
99US-00226012.
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                                                                                                                                                                                                           long QT syndrome; LQT syndrome; gene therapy; human;
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Best Local
                        sequence. The invention is used to diagnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is particularly tumor vascularization, a retinopathy, rheumatoid arthritis, Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis, endometriosis associated with neovascularization, restenosis due to angioplasty, overproduction of tissue due to cicatrisation, a peripheral vascular disease, hypertension, vascular inflammation, Raynaud disease, aneurism, arterial restenosis, thrombophlebitis, ischemia, angina, myocardial infarction, chronic heart disease, cardiac congestion or
                                                                                                                                                                                                                                                                                       The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumor vascularization; retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis; ovary hyperstimulation; psoriasis; endometriosis; restenosis; angioplasty; cicatrisation; peripheral vascular disease; hypertension; vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis; ischemia; angina; myocardial infarction; chronic heart disease; cardiac congestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
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gene therapy; angiogenesis; endothelial cell; diagnosis;
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Pred. No. 2.7;
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                                                                                       The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide sequence. The invention is used to diagnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is particularly tumor vascularization, a retinopathy, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; primer; vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal; antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy; angiogenesis; endothelial cell; diagnosis; tumor vascularization; retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis; ovary hyperstimulation; psoriasis; endometriosis; restenosis; angioplasty; cicatrisation; peripheral vascular disease; hypertension; vascular inflammation; payand's disease; aneurism; thrombophlebitis; ischemia; angina; myocardial infarction; chronic heart disease; cardiac congestion;
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                          Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis, endometriosis associated with neovascularization, restenosis due to angioplasty, overproduction of tissue due to cicatrisation, a periphera vascular disease, hypertension, vascular inflammation, Raymaud disease, vascular disease, hypertension, vascular inflammation, Raymaud disease,
                                                                                                                                                                                                                                                                                  Compositions containing nucleic acid or polypeptide differentially expressed in angiogenesis are useful to diagnose, prognose and treat angiogenic disorders including tumor vascularization and heart disease.
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aneurism, a myocardial
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                  The invention relates to a novel inhibitor of angiogenesis comprising a active substance chosen from at least one of a nucleic acid molecule, a antisense nucleic acid molecule, a polypeptide or an antibody. The invention further comprises: an antisense nucleic acid sequence chosen from any of the sequences provided in the specification; preparation of the antibody comprising in vivo or in vitro immunisation of an immunocompetent animal cell, preferably of a vertebrate and most preferably of a mammal, with at least one of the polypeptide sequences chosen from a sequence provided in the specification; a mammalian expression vector comprising at least one antisense sequence chosen from the control of the polypeptide sequences and sequence chosen from the specification; a mammalian comprising at least one antisense sequence chosen from the specification of the polypeptide sequences appression vector comprising at least one antisense sequence chosen from the specification of the polypeptide sequences appression vector comprising the sequence chosen from the specification of the polypeptide sequences appression vector comprising the sequence sequence chosen from the specification of the polypeptide sequences chosen from the sequence chosen from the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; antisense gene therapy; tumour vascularisation; retinopathies; rheumatoid arthritis; Crohn's disease; atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis; restenosis; tissue granulation; peripheral vascular disorder; hypertension; vascular inflammation; Raynaud's disease; aneurism; arterial restenosis;
                                                                                                                                                                                                                                                                                                                                                    atherosclerosis and
                                                                                                                                                                                                                                                                                                                                                                 Antisense nucleic molecule useful as inhibitor of angiogenesis in treatment of angiogenic disorders, e.g., rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-216677/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-2002; 2002FR-00002717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2003; 2003FR-00007507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        macular degeneration; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myocardial infarction; chronic heart disease; congestive heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibitor; angiogenesis; antisense nucleic acid; immunisation; angiogenic disorder; antiangiogenic; angiogenesis stimulator; dermatological; antiarthritic; antirheumatic; antiinflammatory; vasotropic; hypotensive; opthalmological; antipsoriatic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP73300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        macular degeneration due to age or osteoporosis. This sequence corresponds to a PCR primer to amplify a differentially expressed DNA used in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FR2843753-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP73300 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
  antisense nucleic acid provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENE S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCCCGTCAAGGGCACTCT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCCCGTCACGCGCACTCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector with human antisense DNA insert, GV29-1.
                                                                                                                                                                                                                                                                                                   SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 4 A; 10 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                   ð
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                                                                                                                                                                                                                                                                                                                                                    endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                              404pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.8; DB 17
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                   French
     in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
antisense seque specification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                            sequence chosen from
     preparation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         angina
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RESULT 5
ADK60255/c
ID ADK602
XX ADK602
XX ARTISE
AC ARTISE
XX VASOLI
E ARTISE
XX VASOLI
KW ARGIO
KW ARGIO
KW ARGUL
KW A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis, Crohn's disease, atherosclerosis, ovarian's hyperstimulation, psoriasis, endometriosis associated with neovascularisation, restenosis due to balloon angioplasty, tissue granulation due to scarification, peripheral vascular disorders, hypertension, vascular inflammation, Raynaud's disease, aneurism, arterial restenosis, thrombophlebitis, lymphadenopathy, lymphedema, ischaemia, angina, myocardial infarction, chronic heart disease, congestive heart disease, macular degeneration linked to age and osteoporosis. This polynucleotide sequence represents a primer used the execution of the confidence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal; antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy; angiogenesis; endothelial cell; diagnosis; tumor vascularization; retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis; ovary hyperstimulation; psoriasis; endometriosis; restenosis; ovary hyperstimulation; psoriasis; endometriosis; restenosis; angioplasty; cicatrisation; peripheral vascular disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory, vasotropic, hypotensive, opthalmological, antipsoriatic, and cardiant. The novel nucleic acid molecules of the invention may be used to treat disorders in gene therapy and antisense gene therapy. The nucleic acid sequences, proteins and antibodies as pa of the therapeutic compositions are useful in treating a disorder of angiogenesis chosen from: tumour vascularisation, retinopathies, angiogenesis chosen from: tumour vascularisation, retinopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetically modified cell, that over- or under-expresses a gene implicated in an angiogenic disorder, comprising inserting the vector from above into a mammalian cell; a genetically modified cell that over-expresses or under-expresses at least one gene involved in angiogenesis by a nucleic acid sequence chosen from any of ADP73049 to ADP7338, as the antisense nucleic acid selection of above, or a fragment of any of these; preparation of a cell line that stably expresses an expression vector. The angiogenesis inhibitor has the following activities:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK60255 standard; DNA; 564 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiangiogenic, angiogenesis stimulator, angiogenesis inhibitor, cytostatic, dermatological, antiarthritic, antirheumatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK60255;
                                                                                                                                                                                                                                                                   04-MAR-2002; 2002FR-00002717
                                                                                                                                                                                                                                                                                                                                                   11-APR-2002; 2002FR-00004546
                                                                                                                                                                                                                                                                                                                                                                                                                                        05-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FR2836687-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis; ischemia; angina; myocardial infarction; chronic heart disease;
                                                                                                                                                                                  (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
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                                                                                                                                                                              GENE SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                      AL MAHMOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          congestion; macular degeneration; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCCCGTCACGCGCACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 4 A; 10 C; 10 G; 5 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to angiogenesis differentially expressed GS-N29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 Other;
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Colin S,

Schneider C,

Al Mahmood S;

2004-013912/02

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
ADK60556/c
                                                                                                                                                                                                                                                        vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal; antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy; angiogenesis; endothelial cell; diagnosis; tumor vascularization; retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis; ovary hyperstimulation; psoriasis; endometriosis; restenosis; angioplasty; cicatrisation; psoriasis; endometriosis; restenosis; angioplasty; cicatrisation; psoriasis; angioplasty; cicatrisation; psoriasis; twascular disease; hypertension; vascular inflammation; Raynaud's disease; aneurism; thrombophiebitis; ischemia; angina; myocardial infarction; chronic heart disease; ischemia; angina; myocardial infarction; chronic heart disease;
                                           (GENE-)
              Colin S,
                                                                                                                     04-MAR-2002;
                                                                                                                                                     05-SEP-2003.
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    Antisense DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK60556
                                            GENE SIGNAL.
                                                                                                                                                                                                                                              congestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; 564 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTCCCGTCAAGGGCACTCT 545
              Schneider C,
                                                                                                                       2002FR-00002717.
                                                                                         2002FR-00002717
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                   to angiogenesis differentially expressed GS-N29
                                                                                                                                                                                                                                              macular degeneration;
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               A
                 Mahmood
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ADP73179/c
ID ADP73179;
XX XDP73179;
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibitor; angiogenesis; antisense nucleic acid; immunisation; angiogenic disorder; antiangiogenic; angiogenesis stimulator; cytostatic; dermatological; antiarthritic; antirheumatic; antiinflammatory; vasotropic; hypotensive; opthalmological; antipsoriatic; cardiant; gene therapy; antisense gene therapy; tumour vascularisation; retinopathies; rheumatoid arthritis; Crohn's disease; atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis; restenosis; covarian hyperstimulation; psoriasis; endometriosis; restenosis; tissue granulation; peripheral vascular disorder; hypertension; vascular inflammation; Raynaud's disease; aneurism; arterial restenosis; vascular inflammation; Raynaud's disease; aneurism; arterial restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endometriosis associated with neovascularization, restenosis due to angioplasty, overproduction of tissue due to cicatrisation, a periphera vascular disease, hypertension, vascular inflammation, Raynaud disease, aneurism, arterial restenosis, thrombophlebitis, ischemia, angina, myocardial infarction, chronic heart disease, cardiac congestion or macular degeneration due to age or osteoporosis. This sequence corresponds to an antisease DNA sequence to a differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis comprising an endothelial cell nucleic acid whose expressis induced by an angiogenic factor and inhibited by an angiostatic ager or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression the nucleic acid or a molecule which binds to the polypeptide sequence. The invention is used to disgnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is
                                                                                                                                                                                                                                                                                                                                                                                                                         myocardial infarction; chronic heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particularly tumor vascularization, a retinopathy, rheumatoid arthritis, Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,
                                                                                          04-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                             macular degeneration; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiogenesis inhibitor human DNA antisense region of
                                                                                                                                                   20-JUN-2003; 2003FR-00007507.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTCCCGTCAAGGGCACTCT 545
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                                                                                             2002FR-00002717
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                                                                                                                                                                                                                                                                                                                                                                                                   88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G; 144 T; 0 U;
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Query Match Best Local Matches

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Mismatches 16.8; No. 1. <u>ი</u>

Indels Length 564; 0 Other;

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Similarity

84.0%; A; 164

Pred. Score

2e+02; DB 12; 2;

Sequence

564

B₽;

138

C; 118

144 T; 0 U;

The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide sequence. The invention is used to diagnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is particularly tumor vascularization, a retinopathy, rheumatoid arthritis, Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis, endometriosis associated with nevvascularization, restenosis due to

Claim 4; SEQ ID NO 131; 424pp; French

Compositions for diagnosing, prognosing and treating angiogenic disorders including tumor vascularization and heart disease, comprise nucleic acid

Compositions containing nucleic acid or polypeptide differentially expressed in angiogenesis are useful to diagnose, prognose and treat angiogenic disorders including tumor vascularization and heart disease.

WPI; 2004-013911/02

polypeptide differentially expressed in angiogenesis.

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angioplasty, overproduction of tissue due to cicatrisation, a peripheral vascular disease, hypertension, vascular inflammation, Raynaud disease, aneurism, arterial restenosis, thrombophlebitis, ischemia, angina, myocardial infarction, chronic heart disease, cardiac congestion or macular degeneration due to age or osteoporosis. This sequence corresponds to an antisense DNA sequence to a differentially expressed DNA used in the composition of the invention.

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invention may be used to treat disorders in gene therapy and antisense gene therapy. The nucleic acid sequences, proteins and antibodies as pariof the therapeutic compositions are useful in treating a disorder of angiogenesis chosen from: tumour vascularisation, retinopathies, rheumatoid arthritis, Crohn's disease, atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis associated with neovascularisation, restencesis due to balloon angioplasty, tissue granulation due to scarification, peripheral vascular disorders, hypertension, vascular inflammation, Raynaud's disease, aneurism, arterial restencess, thrombophlebitis, lymphadenopathy, lymphedema, ischaemia, angina, myocardial infarction, chronic heart disease, congestive heart disease, macular degeneration linked to age and osteoporosis. This polymucleotide represents a human antisense DNA region for the creation of an angiogensis inhibitor of the invention.
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expresses or under-expresses at least one gene involved in angiogenesis by a nucleic acid sequence chosen from any of ADP73349 to ADP73338, as the antisense nucleic acid selection of above, or a fragment of any of these; preparation of a cell line that stably expresses an expression vector. The angiogenesis inhibitor has the following activities:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chosen from a sequence provided in the specification; a mammalian expression vector comprising at least one antisense sequence chosen from an antisense nucleic acid provided in the specification; preparation of genetically modified cell, that over- or under-expresses a gene implicated in an angiogenic disorder, comprising inserting the vector from above into a mammalian cell; a genetically modified cell that over-
ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic; anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy; vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
                                                                       Human gene of the invention NOV43b SEQ ID NO:999.
                                                                                                                                              ADH72103
                                                                                                                                                                                ADH72103 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiangiogenic, angiogenesis stimulator, angiogenesis inhibitor, cytostatic, dermatological, antiarthritic, antirheumatic, antiinflammatory, vasotropic, hypotensive, opthalmological, antipsoriatic, and cardiant. The novel nucleic acid molecules of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunocompetent animal cell, preferably of a vertebrate and most preferably of a mammal, with at least one of the polypeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense nucleic molecule useful as inhibitor of angiogenesis in treatment of angiogenic disorders, e.g., rheumatoid arthritis, atherosclerosis and endometriosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  active substance chosen from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense nucleic acid molecule, a polypeptide or an antibody. The invention further comprises: an antisense nucleic acid sequence chosen
                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n any of the sequences provided in the specification; preparation antibody comprising in vivo or in vitro immunisation of an unocompetent animal cell, preferably of a vertebrate and most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a novel inhibitor of angiogenesis ove substance chosen from at least one of a nucleic acid
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                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       564
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nilarity 90.0%;
Conservative
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                                                                                                                                                                                DNA;
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2002US-038691P

2002US-0386931P

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2002US-0386971P

2002US-0387630P

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2002US-0387634P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The invention relates to a novel isolated polypeptide (NOVX). A CC polypeptide of the invention has cytostatic, immunomodulator, comprehenced the invention has cytostatic, immunomodulator, and comprehenced the invention has cytostatic, immunomodulator, and comprehenced the invention of the comprehenced comprehenced by novel per therapy, and as a constant of the polypeptides are encoded by NoVX polymucleotides comprising comprehenced the polypeptide is useful in the manufacture of a comprehenced the comprehenced the manufacture of a complete the comprehenced the polypeptide is useful in the manufacture of a complete the comprehenced the compr
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                                                                                                                                                                         ACA10119 standard; cDNA;
                                      Human NOVX polynucleotide #9
                                                                                      02-JUN-2003
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DB; ADH72104.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides and nucleic acid molecules useful for preventing NOVX-associated disorders, e.g. cancer, diabetes, infection or and in chromosome mapping, tissue typing or pharmacogenomics.
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                                                                                                                                                                                                                                                                                    GGTCCCGTCAAGGGCACTCT 1278
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2002US-0414801P.
2002US-0414840P.
2002US-0417486P.
2002US-0417406P.
2002US-04217406P.
2002US-0421569.
2002US-04221569.
2002US-0422130P.
2002US-0423730P.
2002US-0423739P.
2002US-0425453P.
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llarity 90.0%;
Conservative
                                                                                    (first entry)
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Pred. No. 1.3e
0; Mismatches
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Shimkets RA;
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18-MAY-2001;
21-MAY-2001;
22-MAY-2001;
22-MAY-2001;
23-MAY-2001;
30-MAY-2001;
31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                      18-JUN-2001
31-JUL-2001
17-AUG-2001
21-AUG-2001
21-AUG-2001
17-SEP-2001
17-SEP-2001
27-SEP-2001
27-SEP-2001
27-SEP-2001
27-SEP-2001
27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAY-2001;
16-MAY-2001;
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07-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                 2001US-0291189P.
2001US-02920143P.
2001US-029201P.
2001US-0292374P.
2001US-0293107P.
2001US-0294110P.
2001US-0294827P.
2001US-0294827P.
2001US-0294827P.
2001US-0313389P.
2001US-03133851P.
2001US-03133851P.
2001US-03123873P.
2001US-03123873P.
2001US-0312873P.
2001US-0322701P.
2001US-0325314P.
2001US-0325314P.
2001US-0325314P.
2001US-0325314P.
2001US-032531882P.
2001US-033682P.
2001US-033682P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene; ss; metabolic disorder; diabetes; infectious
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CURAGEN CORP.

Kekuda R, Le Millet I, Pa Shimkets RA, Zerhusen BD; Alsobrook JP, Anderson DW, Boldog FL, Bur Chapoval A, Edinger S, Gerlach V, Gorman Kekuda R, Lepley DM, Li L, Liu X, Malyar Millet I, Padigaru M, Patturajan M, Pena Shimkets RA, Spytek KA, Taupier RJ, Verne Gorman L, Gunther E, Guo X;
Malyankar UM, Miller CE;
Pena CEA, Rieger DK, Shenvernet CAM, Voss EZ; Burgess œ, Casman Shenoy SG;

WPI; 2003-103512/09. P-PSDB; ABU69134.

New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, osteoarthritis, obssity, atherosclerosis, cancer, Parkinson's မ္ပ infections for e.g. disease,

Claim 20; Page 100-101; 340pp; English

The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The sequences are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular disorders (e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g. hypertension, atherosclerosis), previously, immune disorders, alzheimer's disease, Parkinson's disease), epilepsy, immune disorders, bind of a

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RESULT 10
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03-JUN-2002

04-JUN-2002

05-JUN-2002

06-JUN-2002

06-JUN-2002

06-JUN-2002

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07-JUN-2002

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11-JUN-2002

11-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2004
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18; Conserv
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2002US-0385120P.
2002US-0386041P.
2002US-0386047P.
2002US-0386454P.
2002US-0386454P.
2002US-0386454P.
2002US-03867016P.
2002US-0386716P.
2002US-0386971P.
2002US-0386971P.
2002US-0386971P.
2002US-0386971P.
2002US-0387654P.
2002US-0387654P.
2002US-0387668P.
2002US-0387933P.
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treating obesity,

polypeptides and nucleic acid molecules useful for preventing NOVX-associated disorders, e.g. cancer, diabetes, infection or and in chromosome mapping, tissue typing or pharmacogenomics.

o

Rastelli L; Σ,

Example 43; SEQ ID

ö 997;

1880pp; English

New NOVX

The invention relates to a novel isolated polypeptide (NOVX). polypeptide of the invention has cytostatic, immunomodulator,

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17-JUN-2002

18-JUN-2002

19-JUN-2002

19-JUN-2002

19-JUN-2002

10-AUG-2002

09-AUG-2002

09-AUG-2002

12-AUG-2002

12-AUG-2002

12-AUG-2002

13-AUG-2002

13-AU
                                                                                                                                                                                                                                 Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ; Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ella Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdon Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS; Padigaru M, Patturajan M, Pena CEAA, Peyman JA, Raha D, Rass Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA; Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong Thong H;
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P-PSDB; ADH72102.
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2002US-0388026P.
2002US-0389113P.
2002US-0389114P.
2002US-0389146P.
2002US-0389742P.
2002US-0389742P.
2002US-0399742P.
2002US-0399006P.
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2002US-0390209P.
2002US-0401528P.
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2002US-0402381P.
2002US-040343P.
2002US-040343P.
2002US-0403531P.
2002US-041353P.
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2002US-041333P.
2002US-042333P.
2002US-042333P.
2002US-042333P.
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r JR, Edinger SR, Ellerman
Gorman L, Gunther E, Guo )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
16-MAY-2001;
18-WAY-2001;
21-MAY-2001;
22-WAY-2001;
23-MAY-2001;
29-MAY-2001;
30-MAY-2001;
31-MAY-2001;
31-AUG-2001;
21-AUG-2001;
21-AUG-2001;
21-AUG-2001;
21-SEP-2001;
27-SEP-2001;
27-SEP-2001;
27-SEP-2001;
27-SEP-2001;
27-SEP-2001;
27-SEP-2001;
27-SEP-2001;
27-SEP-2001;
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04-MAY-2001;
07-MAY-2001;
14-MAY-2001;
15-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; NOVX; gene; ss; cardiomyopathy; atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes; haemophilia; graft-versus-host disease; AIDS; asthma; Crohn's disease; multiple sclerosis; infection; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
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2001US-028839SP.
2001US-028900PP.
2001US-028900PP.
2001US-0290753P.
2001US-0291249P.
2001US-0292374P.
2001US-0292507P.
2001US-0292507P.
2001US-0294110P.
2001US-0294110P.
2001US-0294110P.
2001US-0313351P.
2001US-0313351P.
2001US-0313851P.
2001US-0313851P.
2001US-032802P.
2001US-032802P.
2001US-0322802P.
2001US-0325632P.
2001US-0325632P.
2001US-0325632P.
2001US-0325632P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8; D: Pred. No. 1.3e 0; Mismatches
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                                                                                                                                                                      Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Casman SJ, Chapoval A, Edinger SR, Gerlach V, Gorman L, Gunther E, Guc Kekuda R, Lepley DM, Li L, Liu X, Malyankar UM, Millet CE, Millet I, Padigaru M, Patturajan M, Pena CEA, Rieger DK, Sł Shimkets RA, Spytek KA, Taupier RJ, Vernet CAM, Voss EZ; Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, tissue typing atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
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(BOLD/)
(BURG/)
(CASM/)
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(CORM/)
(GORM/)
(GORM/
                                                                                                                                                                    Sequence
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14-DEC-2001;
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  1265
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DB; ADO08271.
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                                                                                  l Similarity
18; Conserv
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BOLDOG F L.
BURGESS C E.
CASMAN S J.
CCHAPOVAL A.
ECHAPOVAL A.
ECHAPOVAL A.
GERLACH V.
GORMAN L.
GORMAN L.
GORMAN L.
GORMAN B.
KEKUDA R.
LEPLEY D M.
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PATTURAJAN M.
PENA C E A.
RIEGER D K.
SHENOY S G.
SHIMKETS R A.
SPYTEK K A.
SPYTEK K A.
TAUPIER R J.
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VOSS E
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MILLER C E
MILLET I.
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                                        GGTCCCGTCACGCGCACTCT
                                                                                  Conservative
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2001US-0340305P.
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                                                                                                                                                                    596 A;
                                                                                                 84.0%;
                                                                                                                                                                      475
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                                                                                                      Score 16.8;
Pred. No. 1.
                                                                                                                                                                    C; 554 G;
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                                                                                    Mismatches
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                                                                                    Gaps
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RESULT 12
ADC30192
CC ADC3089) and the polypeptides they encode (ADC3089) and the polypeptides they encode (ADC3089) and the polypeptides they encode (ADC3089) and the polypeptide of the invention additionally encompasses expression CC vectors and host cells comprising a nucleic acid of the invention; the cells comprising a nucleic acid of the invention; the cerombinant production of a polypeptide of the invention; and methods of polypeptides of the invention; and methods of cells comprising polypeptide of the invention; and methods of cells invention further discloses methods of peventing, treating or cempound which binds to a polypeptide of the invention. The cell invention further discloses methods of peventing, treating or campional antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the cexpression or activity of the polypucleotide and/or polypeptide; and 767 cc contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC3262) and the polypeptides encoded by the contigs (ADC32628 cc and 10 diagnostics, drug screening, forensics, gene mapping, in the constitution of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of consers and products dependent on DNA and amino acid sequences. They are considered the recember of the invention acid sequences. They are considered the polypeptides of the invention are consers. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ulcers; osteoporosis; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to 971 novel human cDNA sequences (ADC29919-
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DB; ADC31163.
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Ghosh M,
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Wang D,
Drmanac R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274; 1185pp; English
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Ma Y, A
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Asundi V,
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Weng G;
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RESULT 13
ADL63644
ID ADL63
Covarian cancer cells as compared to their expression in normal (i.e. non-concerned) ovarian cells. The invention also relates to polypeptides concerous) ovarian cells. The invention also relates to polypeptides concoded by the markers, antibodies that selectively bind to the concoded by the markers, antibodies that selectively bind to the concoded by the markers, antibodies that selectively bind to the concoded by the markers, antibodies that selectively bind to the concoded of the patient at risk concoded of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the concoded of the patient an antisense oligonucleotide complementary to a marker of the convention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the compression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed complex to a secreted protein or to a transcribed complex to a secreted protein or to a transcribed comparing the level of expression of the marker is secreted protein or to a transcribed complex to the 
                  CCCCCCCCCCCCCCCXgXg7qqxxgXqXqxqxqXqXqXqXqXqXqXqXqXqXqXq
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25-MAY-2000;
15-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are also useful in generating antarouster, we measure a specificall and as food supplements. The present sequence represents a specificall claimed human cDNA sequence of the invention. Note: The sequence data this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecules (markers) overexpressed in cancer cells as compared to their normal non-cancerous ovarian of used to characterize stage, grade, histological type of ovarian of the compared to characterize stage, grade, histological type of ovarian of the compared to the compared 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-611502/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL63644 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCCTGTCAGGCGCACTCT 546
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2000US-02011940P.
2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
2000US-0257672P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO 21856; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREDICTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid markers which are overexpressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      696 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ovarian cells
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specifically
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RESULT 14
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Matches 18
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                         sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also use in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is
                                                                                                                                                                                                                                                                                      diagnostics, forensics, responsible for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                                               The invention relates to isolated sequences. (I) is useful as hybrid
                                                                                                                                                                                                                        Claim 1; SEQ ID
                                                                                                                                                                                                                                                                       biodiversity.
                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-)
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for generating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
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2000US-00649167.
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medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                        3924;
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                                                                                                                                                                                                                     103pp; English.
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); Mismatches
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     against it,
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                                                                                                                                                 polynucleotide (I) and polypeptide (II)
disation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1035 T;
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     detecting
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This sequence encodes a human thrombospondin protein, BTL.012. A of this protein, comprising a thrombospondin repeat domain, may to modulate angiogenesis at a site. The BTL.012 fragment may be diagnosing, preventing or treating a medical condition, particul

BTL.012. A main, may be us nt may be used , particularly

fragment be used

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                         Chen J, Chen D, Zo
Dubois-Stringfellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; thrombospondin; BTL.012; thrombospondin repeat domain; modulation; angiogenesis; cancer; metastasis; diabetic retinopathy; macular degeneration; cardiovascular disease; wound; ss.
                                                                                                                                    Claim
                                                                                                                                                                            angiogenesis, and is macular degeneration,
                                                                                                                                                                                                             Novel protein designated BTL.012 has angiogenesis, and is useful to treat
                                                                                                                                                                                                                                                                                           P-PSDB;
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ALIGNMENTS

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1 (bases 1 to 20)
Keating,M.T. and Splawski,I.
Keating,M.T. and splawski,I.
Mutations in and genomic structure of HERG--a long QT syndrome Mutations in 207383-A 60 27-MAR-2001;
Patent: US 6207383-A 60 27-MAR-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60
AR139543
AR139543.1
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                       BD223632
BD223632.1 GI:33033402
JP 2002521065-A/58.
Homo sapiens (human)
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Larity 100.0%; Pred. No. 1.6e+02;
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UNIVERSITY OF UTAH RESEARCH FOUNDATION
OS Homo sapiens (human)
PN JP 2002521065-A/58
PD 16-JUL-2002
PF 20-JUL-1999 UF 2000562554
PF 27-JUL-1999 US 09/122847,06-JAN-1999 US
WARK T KEATING, JGOR SPLAWSKI
PC C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 20)
Keating, M.T. and Splawski
Mutations in and genomic
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Sequence 60 from Patent
CS124258
CS124258.1 GI:71057341
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                                                Similarity 20; Conserv
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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  GGTCCCGTCACGCGCACTCT
                     GGTCCCGTCACGCGCACTCT
                                                                                                                                                             ent: EP 1553190-A 60 13-JUL-2005;
University of Utah Research Foundation
Location/Qualifiers
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                                               100.0%; Score 20; DB 6; llarity 100.0%; Pred. No. 1.6e+02; Conservative 0; Mismatches 0;
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Pred. No. 1.6e+02;
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Best Local S
Matches 17
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papillionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                    79136 bp DNA Lotus corniculatus var. japonicus clone PROGRESS ***, 21 unordered pieces. AP007610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-MAY-2003) Shusei Sato, Kazusa DNA Research Institute, Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337), Fax:81-438-52-3934)
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Lotus corniculatus var. japonicus clone:LJT39K18, TM0252c, complete
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                                                                                                                                                   APO07610.1 GI:56805923
HTG; HTGS_PHASE1.
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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17; Conserv
            Unpublished
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                                                                   Structural
                                                                                         Kaneko, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCCGTCACGCGCACTC
(bases 1 to 79136)
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                                           and Mapping
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                                        Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Analysis of a Lotus japonicus Genome. XI. Sequence
nd Mapping of Nine hundred twenty-one TAC Clones
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2.2e+03;
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clone="LjT11B21"
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22509: contig of 4061 bp in length
22609: gap of unknown length
25097: contig of 2488 bp in length
25097: contig of 2488 bp in length
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30249: gap of unknown length
3050: gap of unknown length
34950: contig of 4701 bp in length
35050: gap of unknown length
40867: contig of 5817 bp in length
47770: contig of 6803 bp in length
47870: gap of unknown length
47870: gap of unknown length
54765: contig of 6895 bp in length
54865: gap of unknown length
75900: contig of 21035 bp in length
76000: gap of unknown length
79136: contig of 3136 bp in length
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                                                                                Submitted (26-MAR-2002) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:yn@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                               DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:yn@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81.478-67-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T., Sato,S. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Sixty-six TAC clones which cover the 6.7 Mb Regions of the Genome
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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Lotus corniculatus var. japonicus
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Submitted (26-MAR-2002) Yasukazu Nakamura,
             AP007711
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/note="TAC clone:TM0024
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/chromosome="2"
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Pred. No. 1.6e+0
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Pred. No. 1.6e+03;
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/variety="japonicus"
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PROGRESS ***, 19 unordered pieces.
AP007711
AP007711 GI:56806021
HTG; HTGS PHASE1.
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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* NOTE: This is a 'working draft' sequence. It currently

* consists of 19 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown

* This record will be updated with the finished sequence
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Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research I Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research I Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Chiba, 292-0818, Japan (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko,T., Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. XI. Sequence Structural Analysis of Nine hundred twenty-one TAC Clones
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/organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
                                                                         68389: contig of 8976 bp in length 68489: gap of unknown length 89430: contig of 20941 bp in length 89530: gap of unknown length 9117: contig of 1587 bp in length.
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Lotus corniculatus var. japonicus
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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/clone="LjT25F20"
/clone_lib="LjT library"
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Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Submitted (12-NOV-2003) Shusei Sato, Kazusa DNA Research Institute,
Submitted (12-NOV-2003) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
Fax:81-438-52-3934)
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                                                                                                 synonym: Lotus japonicus"
                                                                                                                                                                                     /mol type="genomic DNA"
/variety="japonicus"
/db_xref="taxon:34305"
/chromosome="3"
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/clone_lib="LjT library"
/note="TAC clone:TM0338, synonym:Lotus japonicus"
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/mol_type="genomic DNA"
/variety="japonicus"
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/note="TAC clone:TM0209
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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85.0%; Score 17; DB 15; 100.0%; Pred. No. 1.5e+03; ive 0; Mismatches 0;
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                                           Length 104684;
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 Kaneko, T.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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                                                                         Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicotyledons;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Lotus corniculatus var. japonicus"
/mol type="genomic DNA"
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e LiT11C12, ***
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* NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Features and Mapping of Unpublished 2 (bases 1 to 108554)
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Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kiss
Chiba, 292-0818, Japan (E-mail:ssatoskazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935 (ex.2337),
Fax:81-438-52-3934)
* NOTE: This is a 'working draft' sequence. It currently
consists of 21 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Direct Submission
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0;
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3336: gap of unknown length
39155: contig of 5819 bp in length
45778: contig of 6523 bp in length
45878: gap of unknown length
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52310: gap of unknown length
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60930: gap of unknown length
60930: gap of unknown length
609310: contig of 8380 bp in length
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18628: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                    AX828485 564 bp DNA Sequence 131 from Patent W003074073. AX828485
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                      GGTCCCGTCACGCGCACTCT 20
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Pred. No. 3.3e+03
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Pred. No. 4.6e+03;
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